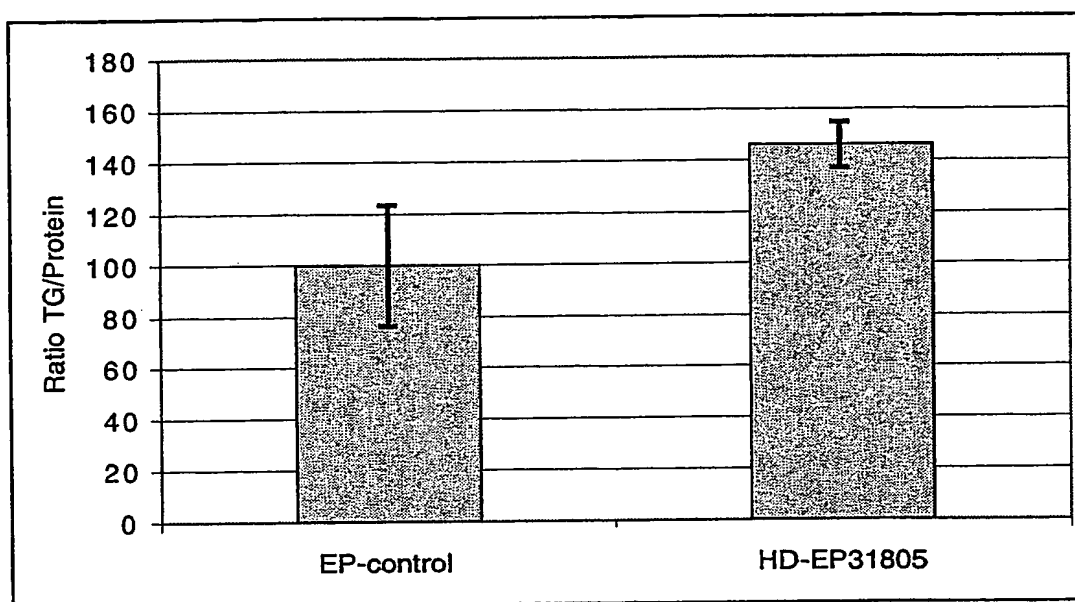


Figure 1. Triglyceride content of a *Drosophila* CG7956 (GadFly Accession Number) mutant



BEST AVAILABLE COPY

Figure 2. Molecular organization of the CG7956 gene (GadFly Accession Number)

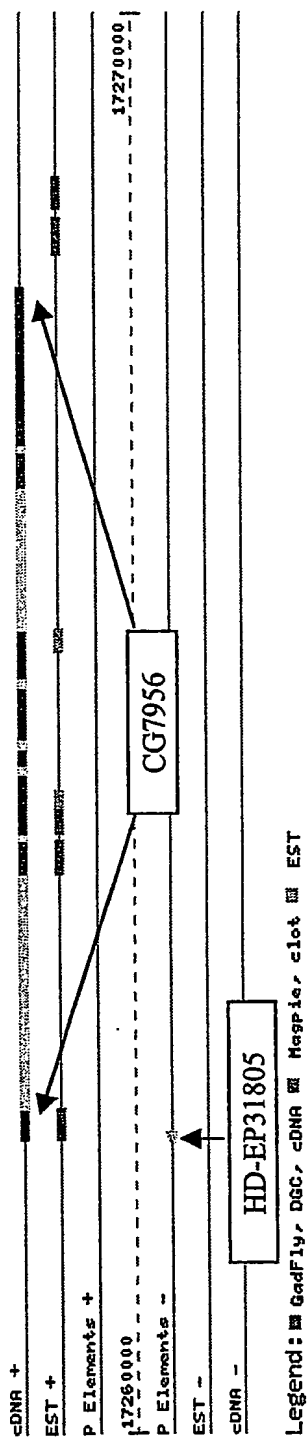


Figure 3. BLASTP results for CG7956 (GadFly Accession Number)**Homology to human protein NP_055752.1 (GenBank Accession Number)**

ref|NP_055752.1| (NM_014937) KIAA0966 protein [Homo sapiens]
Length = 1132

Score = 573 bits (1477), Expect = e-162

Identities = 354/972 (36%), Positives = 514/972 (52%), Gaps = 114/972 (11%)

Query: 1 MEVFQTD SHYIFVKRDKSLWWHRRTSEFSIKAGWDLSSVDDIECIGVTHGIVGVISLPNV 60
ME+FQ HYI + +++LW RR ++ DL + C+G+ G++G I L +
Sbjct: 1 MELFQAKDHYILOQGERALWCSRRDGGQLR PATDLLAWN PICLGLVEGVIGIKIQLHSD 60

Query: 61 YEPHLVVVKEASAVGVLYPPHLVYKI KSICILSADD---PD TDL PNCTKHTKSNQSTPTH 117
L+++++ + VG L H V K+ I +LS + D +L C KH
Sbjct: 61 LPWWLILIRQKALVGKLP GDHEVCKVT KIAVLSLSEMEPQDLELELCCKH----- 110

Query: 118 SVSTSNNNNASVPSSGGGSSKSTKLFEGMKN TWGAVKSAGNT---IKNTTQQAANLATKQ 174
G+NK + S ++ +K T +N++
Sbjct: 111 -----HFGINKPEKIIPSPDDSKFLLKTFTHIKSNVSAPN 145

Query: 175 VKSSVGIREPRHIERRITEELHKIFDETD SFYFSFDCDITNNLQRHEAKSEESQ---SQP 231
K +E +ERR+ EEL K+F +++SFY+S D+TN++QR + + +
Sbjct: 146 KKKVKESKEKEKLEERRLLEELLKMFMDSESFYYSLT YDLTNSVQRQSTGERDGRPLWQKV 205

Query: 232 DERFFWNKHMIRDLINLNDKT---WILPIIQGF MQVENCVIG----- 270
D+RFFWNK+MI+DL + WI+P+IQGF+Q+E V+
Sbjct: 206 DDRFFWNKYMIQDLTEIGTPD VDFWIIPMIQGFVQIEELVVNYTESSDDEKSSPETPPQE 265

Query: 271 NEC-----FTLALVSRRSRHRAGTRYKRRGVDEKGN CANYVETEQILSFRHHQLSFTQ 323
+ C F +AL+SRRSRHRAG RYKRRGVD+ GN ANYVETEQ++ +H LSF Q
Sbjct: 266 STCVDDIHPRFLVALISR SRHRAGMRYKRRGV DKNGNVANYVETEQLIHVHNHTLSFVQ 325

Query: 324 VRGSVPIYWSQPGYKYRPPRLDRGVAETQQA FELHFTKELETYGRVCIVNLVEQSGKEK 383
RGSVP++WSQ GY+Y P PRLDR ET F HF ++L Y + I+NLV+Q+G+EK
Sbjct: 326 TRGSVPVFWSQVGYRYNPRPRLDRSEKETVAYFCAHFEEQLNIYKKQVIINLVDQAGREK 385

Query: 384 TIGDAYADHVIKLNNDR LIYVTFDFHDYCRGMR FENV SALIDAVGPEAGAMGFHWRDQRG 443
IGDAY V+ NN L YV+FDH++CRGM+FENV L DA+ M + W D+ G
Sbjct: 386 IIGDAYLKQVLLFNNSHLTYVS FDFHEHCRGMKFENVQTLTDAIYDIILDMKWCWVDEAG 445

Query: 444 MICNQKSVFRVNCMDCLDR TNVVQTAIGKAVLESQ LVKLGLSPPYTP IPEQLKSPFMVLW 503
+IC Q+ +FRVNCMDCLDR TNVVQ AI + V+E QL KLG+ PP P+P + + ++W
Sbjct: 446 VICKQEGIFRVNCMDCLDR TNVVQA A IARV VMEQQLKKGVMPP EQPLPVKCNRIYQIMW 505

Query: 504 ANNGDIISRQYAGTNALKG DYTRTGERKISGM MKDGMNSANRYYLARFKDSYRQATIDLM 563
ANNGD ISRQYAGT ALKGD+TRTGERK++G+MKDG+NSANRYYL RFKD+YRQA IDLM
Sbjct: 506 ANNGDSISRQYAGTAALKGDFTRTGERKLAGVMKDG VNSANRYYLNRFKDAYRQAVIDLM 565

Query: 564 LGNQVSSESLSALGGQAGPD---ENDGTENAEQAKLLVEDCRRL LLGTAQYPVGAWGLID 620
G V+ + S + + + + + E L++ +LLL + G W LID
Sbjct: 566 QGIPVTEDLYSIFTKEKEHEALHKNQRSHQELISQLLQSYMKLLLPDDEKFHGGWALID 625

Query: 621 ADPSSGDINETEVD TILLTDDCYIVA EYDSHLDKIVRFEKVQLTQVR LIELGMHQQT KI 680
DPS D +VD +LLL++ Y VA YD +DK+ +++++ L + IE+G + +
Sbjct: 626 CDPSLIDATHRDVDV LLLL SNSAYYVAYYDDEVDKVNQYQRLSLENLEKIEIG--PEPTL 683

Query: 681 FQGSAPAHLCRLNYSVDEQEGYFHMFRSANLRFFNNMAYVIKTQEEVAESMTSIVEMFR 740
 F P C+RL+Y E GYFH R A + +E+ +++ I EM +
 Sbjct: 684 F--GKPKFSCMRLHYRYKEASGYFHTLR-----AVMRNPEEDGKDTLQCIAEMLQ 731

Query: 741 IALDNAGNTEVRYITGGVLQRRKSKLPTLDV-----PRGMPRNLSSESQLVQLSSKA 791
 I G+ I L+R+ SK P D+ +N S+ L+ K
 Sbjct: 732 ITKQAMGSD--LPIIEKKLERKSSK-PHEDIIGIRSQNQGSQAQGNFLMSKFSSSLNQKV 788

Query: 792 LSNMA----GQFSKLGQTFKKPQAHPPSSLAATMNPQVMRQDSEIESGQEAQKAVFTLGR 847
 + G KLG F KP+ + L + + + DS +E+ + V +
 Sbjct: 789 KQTKSNVNIGNLRKLG-NFTKPEMKVNFLKPNLKVNLWKS-DSSLETMENT--GVMDKVQ 844

Query: 848 KHRNSNSASSTDTDEHDNSLYEPEVDSDEIAMDKSNYNE-NAFLPSVGIVMG----NQK 902
 + + +S D+ D L + D D ++A + + LPS GI+ +
 Sbjct: 845 AESDGDMSDDNDSDYHSDEFLTNSKSDEDRQLANSLESVGPIDYVLPSCGIIASAPRLGSR 904

Query: 903 EDSPSSSDEIRH 914
 S SS+D H
 Sbjct: 905 SQSLSSTDSSVH 916

Figure 4. Expression of the CG7956 Homologs in Mammalian Tissues

Figure 4A. Real-time PCR analysis of Sac domain-containing inositol phosphatase 2 (SAC2) expression in wild type mouse tissues

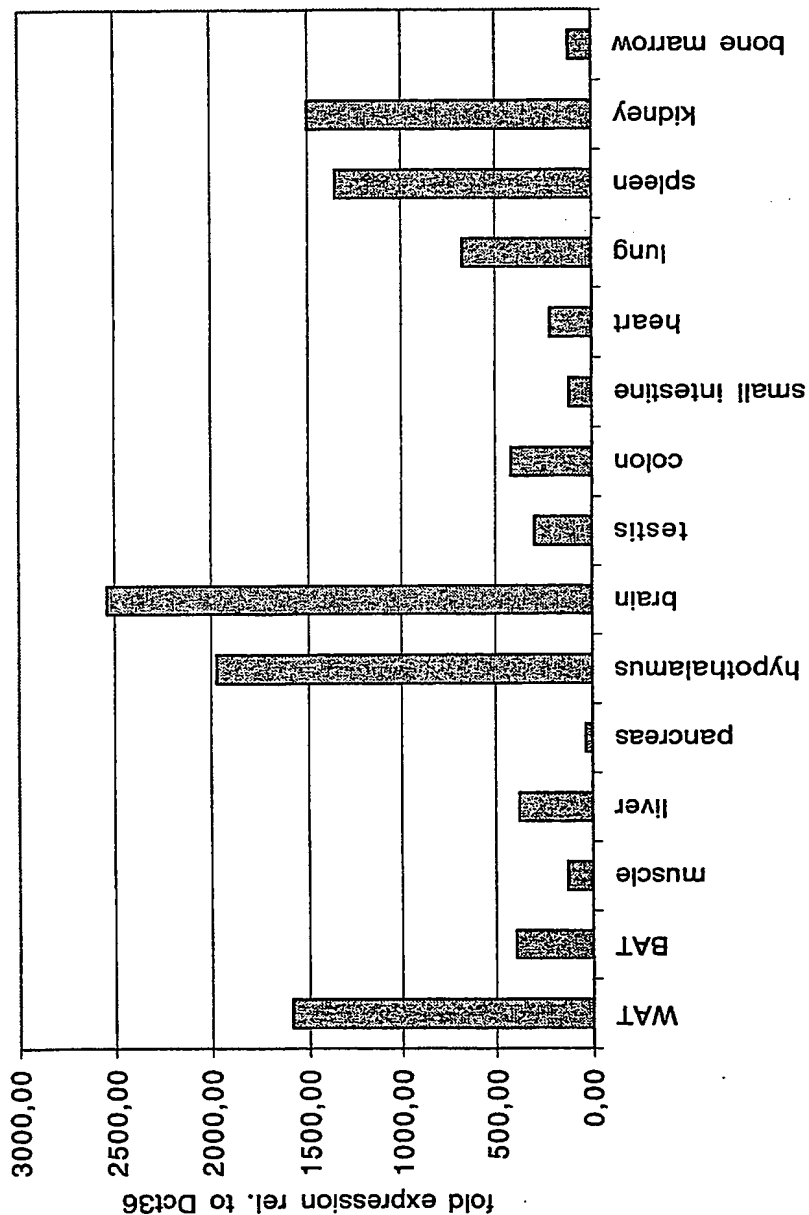


Figure 4B. Real-time PCR analysis of Sac domain-containing inositol phosphatase 2 (SAC2) expression in different mouse models

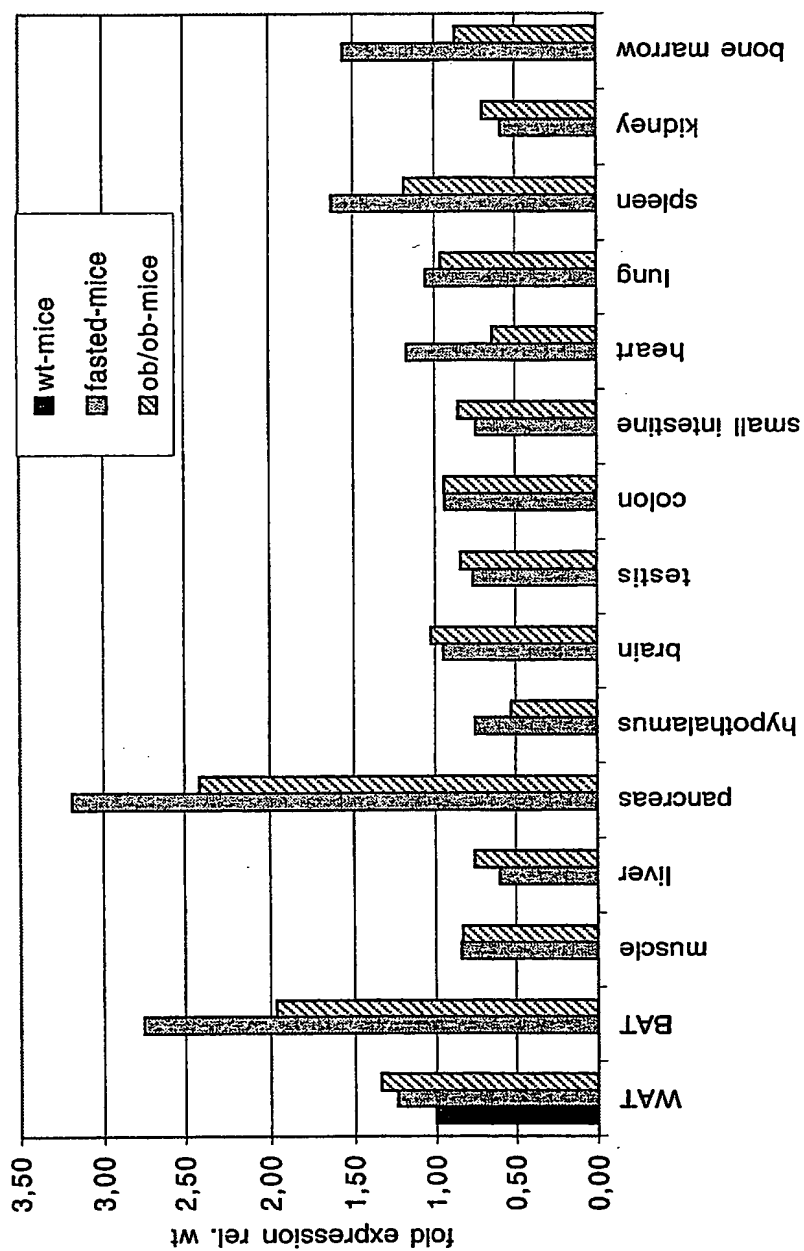


Figure 5. Triglyceride content of a *Drosophila aralar 1* (GadFly Accession Number CG2139) mutant

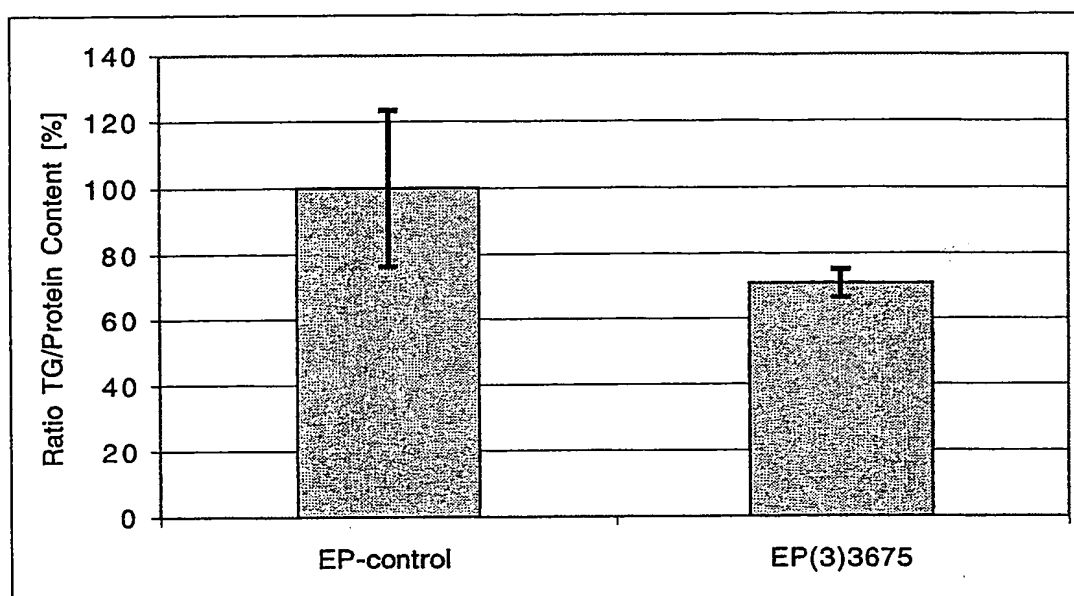


Figure 6. Molecular organisation of the *aralar 1* gene (GadFly Accession Number CG2139)

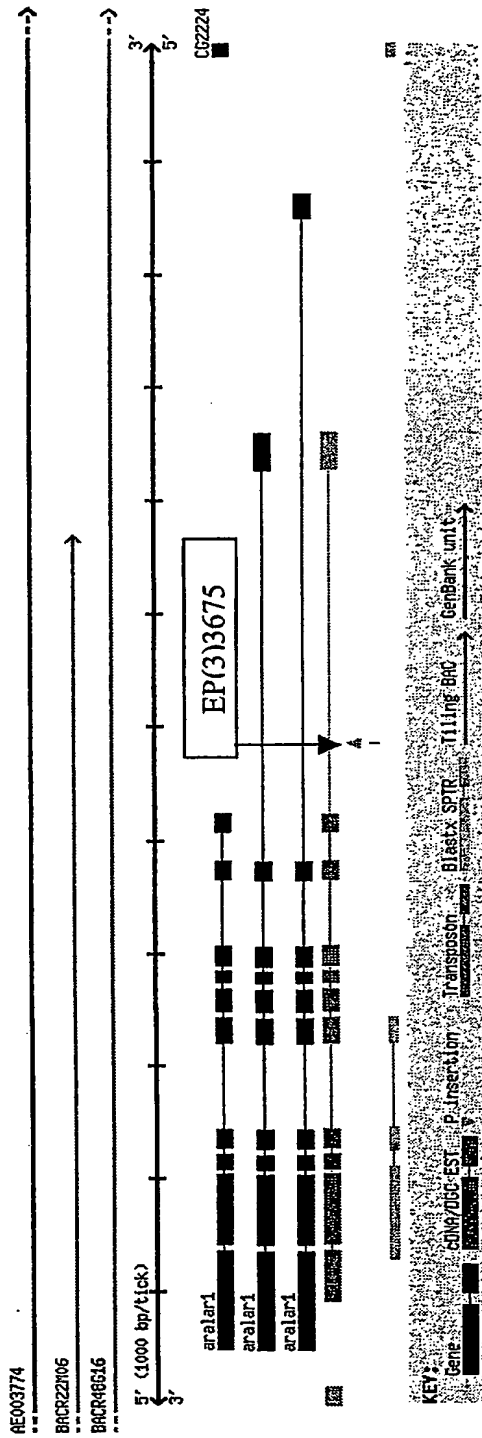


Figure 7. Homology of *Drosophila aralar 1* (GadFly Accession Number CG2139) to human solute carrier family 25, members 12 and 13

**Figure 7A. BLASTP results for *alarar 1*
Homology to human protein XP_010876.3 (GenBank Accession Number)**

ref|XP_010876.3| (XM_010876) solute carrier family 25 (mitochondrial carrier, Aralar), member 12 [Homo sapiens]
Length = 678

Score = 741 bits (1913), Expect = 0.0
Identities = 382/650 (58%), Positives = 488/650 (74%), Gaps = 14/650 (2%)

```

Query: 1  MTSEDFVRKFLGLFSESAFNDESVRLLANIADTSKDGILISFSEFQAFEGLLCTPDALYRT 60
          MT EDFV+++LGL+++ N + V+LLA +AD +KDGLIS+ EF AFE +LC PD+++
Sbjct: 34  MTPEDFVQRYLGLYNDPNSNPKIVQLLAGVADQTKDGLISYQEFALAFESVLCAPDSMFIV 93

Query: 61  AFQLFDRKNGTVSYADFADVQKTELHSKIPFSLDGPFIKRYFGDKKQRLINYAEFTQL 120
          AFQLFD+ GNG V++ + ++ +T +H IPF+ D FI+ +FG +++ +NY EFTQ
Sbjct: 94  AFQLFDKSGNGEVTTFENVKEIFGQTIHHHIPFNWDCEFIRLHFGHNRRKHLNTEFTQF 153

Query: 121  LHDFHEEHAMEAFRSKDPAGTGFISPLDFQDIIIVNKRHLLTPGVRDNLVSVTEG---HK 177
          L + EHA +AF KD + +G IS LDF DI+V ++ H+LTP V +NLVS G H+
Sbjct: 154  LQELQLEHARQAFALKDKSKSGMISGLDFSDIMVTIRSHMLTPFVEENLVSAAAGGSISHQ 213

Query: 178  VSFPHYFIATSLNNMELIKQVYLHATEGSRDMD-ITKDQILLAAQTMSQITPLEIDILF 236
          VSF YF AF SLLNNMEL++++Y G+R D+ +TK++ +A Q+TPLEIDIL+
Sbjct: 214  VSFSYFNAFNSLLNNMELVRKIY-STLAGTRKDVEVTKEEFAQSAIRYGQVTPLEIDILY 272

Query: 237  HLAGAVHQAGRIDYSDLSNIAPEHYTKHMTHLAEIKAVESPA-DRSAFIQVLESSYRFT 295
          LA + +GR+ +D+ IAP + + LAE++ +SP R ++Q+ ES+YRFT
Sbjct: 273  QLADLYNASGRLTLADIERIAPLAEGA-LPYNLAEQRQQSPGLGRPIWLQIAESAYRFT 331

Query: 296  LGSFAGAVGATVVYPIDLVKTRMQNQR-AGSYIGEVAIRNSWDCFKKVVRHEGFMGLYRG 354
          LGS AGAVGAT VYPIDLVKTRMQNQR +GS +GE+ Y+NS+DCFKKV+R+EGF GLYRG
Sbjct: 332  LGSVAGAVGATAVYPIDLVKTRMQNQRGSGSVGELMYKNSFDCFKKVLRYEGFFGLYRG 391

Query: 355  LLPQLMGVAPEKAIKLTVNDLVRDKLTDKKGNIPTWAEVLAGGCAGASQVFTNPLEIVK 414
          L+PQL+GVAPEKAIKLTVND VRDK T + G++P AEVLAGGCAG SQV+FTNPLEIVK
Sbjct: 392  LIPQLIGVAPEKAIKLTVNDVFRDKFTRRDGSLPLAEVLAGGCAGGSQVIFTNPLEIVK 451

Query: 415  IRLQVAGEIASGSKIRAWSVRELGLFGLYKGARACLLRDVPFSAIYFPTYAHTKAMMAD 474
          IRLQVAGEI +G ++ A +V+R+LG+FGLYKGA+AC LRD+PFSAIYFP YAH K ++AD
Sbjct: 452  IRLQVAGEITTGPRVSALNVLRLDLGIFGLYKGAKACFLRDIPFSAIYFPVYAHCKLLLLAD 511

Query: 475  KDGYNHPLTLAAGAIAGVPAASLVTPADVIKTRLQVVARSGQTTYTGVDATKKIMAE 534
          ++G+ L LLAAGA+AGVPAASLVTPADVIKTRLQV AR+GQTTY+GV D +KI+ EE
Sbjct: 512  ENGHVGGNLNLLAAGAMAGVPAASLVTPADVIKTRLQVAARAGQTTYSGVIDCFRKILREE 571

Query: 535  GPRAFVKGTAAARVFRSSPQFGVTLVTYELLQRLFYVDFGGTQPKGSEAHKITTPLEQAAA 594
          GP APWKGTAAARVFRSSPQFGVTLVTYELLQRL FY+DFGG +P GSE TP + A
Sbjct: 572  GPSAFVKGTAAARVFRSSPQFGVTLVTYELLQRLWFYIDFGGLKPAGSE----PTP-KSRIA 626

Query: 595  SVTTENVDHIGGYRAAVPLLAGVESKFGLYLPRF-GRGVTAASPSTATGS 643
          + N DHIGGYR A AG+E+KFGLYLP+F V P A +
Sbjct: 627  DLPPANPDHIGGYRLATATFAGIENKFGLYLPKFKSPSAVVQPKAAVAA 676

```

Homology to human protein NP_055066.1 (GenBank Accession Number)

ref|NP_055066.1| (NM_014251) solute carrier family 25, member 13 (citrin)
[Homo sapiens]
Length = 675

Score = 728 bits (1878), Expect = 0.0
Identities = 374/643 (58%), Positives = 476/643 (73%), Gaps = 17/643 (2%)

Query: 1 MTSEDFVRKFLGLFSESAFNDESVRLLANIADTSKDGLISFSEFQAFEGLLCTPDALYRT 60
M+ DFV ++L +F ES N ++V LL+ + D +KDGLISF EF AFE +LC PDAL+
Sbjct: 35 MSPNDFVTRYLNIFGESQPNPKTVELLSGVVDQTKDGLISFQEFVAFESVLCAPDALFMV 94

Query: 61 AFQLFDRKNGTVSYADFADVVQKTELHSKIPFSLDGPFIKRYFGDKKQRLINYAEFTQL 120
AFQLFD+ G G V++ D V +T +H IPF+ D F++ +FG +++R + YAEFTQ
Sbjct: 95 AFQLFDKAGKGEVTFEDVKQVFGQTTIHQHIFPNWDSEFVQLHFGKERKRHLTYAEFTQF 154

Query: 121 LHDFHEEHAMEAFRSKDPAGTGFISPLDFQDIIVNVKRHLLTPGVRDNLVSVTEG---HK 177
L + EHA +AF +D A TG ++ +DF+DI+V ++ H+LTP V + LV+ G H+
Sbjct: 155 LLEIQLEHAKQAFVQRDNARTGRVTAIDFRDIMVTIRPHVLTPEVECLVAAAGGTTSHQ 214

Query: 178 VSFPYFIAFTSLLNNMELIKQVYLHATEGSRTDM-ITKDQILLAAQTMSQITPLEIDILF 236
VSF YF F SLLNNMELI+++Y G+R D+ +TK++ +LAAQ Q+TP+E+DILF
Sbjct: 215 VSFSYFNGFNLSLLNNMELIRKIY-STLAGTRKDVEVTKEEFVLAAQKFGQVTPMEVDILF 273

Query: 237 HLAGAVHQAGRIDYSDLSNIAP-EHYTKHMTHLAEIKAVESPAD--RSAFIQVLESSYR 293
LA GR+ +D+ IAP E T + LAE + ++ D R +QV ES+YR
Sbjct: 274 QLADLYEPRGRMTLADIERIAPLEEGT--LPFNLAEAQRQKASGDSARPVLLQVAESAYR 331

Query: 294 FTLGSFAGAVGATVVYPIDLVKTRMQNQRA-GSYIGEYAYRNSWDCFKKVVRHEGFMGLY 352
F LGS AGAVGAT VYPIDLVKTRMQNQRA+ GS++GE+ Y+NS+DCFKKV+R+EGF GLY
Sbjct: 332 FGLGSVAGAVGATAVYPIDLVKTRMQNQIRSTGSFVGELMYKNSFDCFKKVLRYEGFFGLY 391

Query: 353 RGLLPQLMGVAPEKAIKLTVNDLVKTRDKLTDKKGNIPTWAEVLAGGCAGASQVFTNPLEI 412
RGLLPQL+GVAPEKAIKLTVND VRDK K G++P AE+LAGGCAG SQV+FTNPLEI
Sbjct: 392 RGLLPQLLGVAPEKAIKLTVNDVFRDKFMHKDGSVPLAAEILAGGCAGGSQVIFTNPLEI 451

Query: 413 VKIRLQVAGEIASGSKIRAWSVRELGLFGLYKGARACLLRDVPFSAIYFPTYAHTKAM 472
VKIRLQVAGEI +G ++ A SVVR+LG FG+YKGA+AC LRD+PFSAIYFP YAH KA
Sbjct: 452 VKIRLQVAGEITTGPRVSALS SVVRDLGFFGIYKGAACFLRDIPFSAIYFPCYAHVKASF 511

Query: 473 ADKDGYNHPLTLAAGAIAGVPAASLVTPADVILKTRQLQVVARSGQTTYTGVDATKKIMA 532
A++DG P +LL AGAIAG+PAASLVTPADVILKTRQLQV AR+GQTTY+GV D +KI+
Sbjct: 512 ANEDGQVSPGSLLLAGAIAGMPAASLVTPADVILKTRQLQVAARAGQTTYSGVIDCFRKILR 571

Query: 533 EEGPRAFWKGTAAARVFRSSPQFGVTLVITYELLQRLFYVDFGGTQPKGSEAHKITTPLEQA 592
EEGP+A WKG ARVFRSSPQFGVTL+TYELLQR FY+DFGG +P GSE P+ ++
Sbjct: 572 EEGPKALWKGAGARVFRSSPQFGVTLITYELLQRFYIDFGGVKPMGSE-----PVPKS 625

Query: 593 AASVTTENVDHIGGYRAAVPLLAGVESKFGLYLPFRFGRGVTA 635
++ N DH+GGY+ AV AG+E+KFGLYLP F V+ +
Sbjct: 626 RINLPAPNPDHVGGYKLAVATFAGIENKFGLYLPFLFKPSVSTS 668

Figure 7B. Multiple Sequence Alignment (ClustalW 1.83)

```

aralar1 Dm  MPLTKSLPNSPSLLKRAGTEKLREVFLKYASIQKNGEHYMTSEDFVRKFLGLFSESFAFND
SLC25A12 Hs  -----MAVKVQTTKRGDPHELRNIFLQYASTEVDGERYMTPEDFVQRYLGLYNDPNSNP
SLC25A13 Hs  -----MAAAKVALTKRADPAELRTIFLKYASIEKNGEFFMSPNDFVTRYLNIFGESQPNP

aralar1 Dm  ESVRLLANIADTSKDGLISFSEFQAFEGLLCTPDALYRTAFQLFDRKGNGTVSYADFADV
SLC25A12 Hs  KIVQLLAGVADQTKDGLISYQEFLLAFESVLCAPDSMFIVAFQLFDKSGNGEVTFFENVKEI
SLC25A13 Hs  KTVELLSGVVDQTKDGLISFQEFVAFESVLCAPDALFMVAFQLFDKAGKGEVTFEDVKQV

aralar1 Dm  VQKTELHSKIPFSLDGPFIKRYFGDKKQRLINYAEFTQLLHDFHEEHAMEAFRSKDPAGT
SLC25A12 Hs  FGQTIIHHHIPFNWDCEFIRLHFHGNRKKHLNYTEFTQFLQELQLEHARQAFALKDKSKS
SLC25A13 Hs  FGQTTIHQHIFPNWDSEFVQLHFGKERKRHLTYAEFTQFLLEIQLEHAKQAFVQORDNART

aralar1 Dm  GFISPLDFQDIIIVNVRHLLTPGVRDNLVSVTEG---HKVSFPYFIAFTSLLNNMELIKQ
SLC25A12 Hs  GMISGLDFSDIMVTIRSHMLTPFVEENLVSAAGGSIHQVSFSYFNAFNSLLNNMELVRK
SLC25A13 Hs  GRVTAIDFRDIMVTIRPHVLTTPFVEECLVAAAGGTTSHQVSFSYFNGFNSLLNNMELIRK

aralar1 Dm  VYLHATEGSRTDMITKDQILLAAQMSQITPLEIDILFHLAGAVHQAGRIDYSDLNIAPI
SLC25A12 Hs  IYSTLAGTRKDVEVTKEEFAQSAIRYQGVTPLEIDILYQLADLYNASGRLTLADIERIAPI
SLC25A13 Hs  IYSTLAGTRKDVEVTKEEFVLAQAQKFGQVTPMEVDILFQLADLYEPRGRMTLADIERIAPI

aralar1 Dm  EHYTKHMTHRLAEIKAVESPA--DRSAFIQVLESSYRFTLGSGFAGAVGATVVYPIDLVKT
SLC25A12 Hs  LAEG-ALPYNLAELQRQQSPG-LGRPIWLQIAESAYRFTLGSGVAGAVGATAVYPIDLVKT
SLC25A13 Hs  LEEG-TLPFNLAEAQRQKASGDSARPVLLQVAESAYRFGLGSGVAGAVGATAVYPIDLVKT

aralar1 Dm  RMQNQR-AGSYIGEVAYRNSWDCFKKVRHEGFMGLYRGLLPQLMGVAPEKAIKLTVNDL
SLC25A12 Hs  RMQNQRGSGSVVGELMYKNSFDCFKKVLRYEGFFGLYRGLIPQLIGVAPEKAIKLTVNDL
SLC25A13 Hs  RMQNQRSTGSGFVGELMYKNSFDCFKKVLRYEGFFGLYRGLLPQLLGVAPEKAIKLTVNDL

aralar1 Dm  VRDKLTDKKGNIPTWAEVLAGGCAGASQVVFTNPLEIVKIRLQVAGEIASGSKIRASVSV
SLC25A12 Hs  VRDKFTRRDGSSVPLPAEVLAGGCAGGSQVIFTNPLEIVKIRLQVAGEITTGPRVSALNVL
SLC25A13 Hs  VRDKFMHKDGSVPLAAEILAGGCAGGSQVIFTNPLEIVKIRLQVAGEITTGPRVSALS SVV

aralar1 Dm  RELGLFGLYKGARACLLRDVPFSAIYFPPTYAHTKAMMADKDGYNHPLTLAAGAIAGVPA
SLC25A12 Hs  RDLGIFGLYKGAKACFLRDIPFSAIYFPVYAHCKLLLADENGHVGGNLLAAGAMAGVPA
SLC25A13 Hs  RDLGFFGIYKGAKACFLRDIPFSAIYFPCYAHVKASFANEDGQVSPGSLLLAGAIAGMPA

aralar1 Dm  ASLVTPADVIRLQVVARSGQTTYTGVDATKKIMAEEGPRAFWKGTAAARVFRSSPQFG
SLC25A12 Hs  ASLVTPADVIRLQVAARAGQTTYSGVIDCFRKILREEGPSAFWKGTAAARVFRSSPQFG
SLC25A13 Hs  ASLVTPADVIRLQVAARAGQTTYSGVIDCFRKILREEGPKALWKAGARVFRSSPQFG

aralar1 Dm  VTLVTYELLQRLFYVDGFGTQPKGSEAHKITTPLEQAAASVTTENVDHIGGYRAAVPLLA
SLC25A12 Hs  VTLVTYELLQRWFYIDFGGLKPKGSEP-----TPKSRIAD-LPPANPDHIGGYRLATATFA
SLC25A13 Hs  VTLLTYELLQRWFYIDFGGVKPMGSEP-----VPKSRIN--LPAPNPDHVGGYKLAVATFA

aralar1 Dm  GVESKFGLYLPRFGRGVTAASPSTATGS---
SLC25A12 Hs  GIENKFGLYLPKFKSPSAVVQPKAAVAATQ
SLC25A13 Hs  GIENKFGLYLPFLK-PSVSTSKAIGGGP---
```

Figure 8. Expression of *aralar 1* Homologs in Mammalian Tissues

Figure 8A. Real-time PCR analysis of Slc25a12 expression in wild type mouse tissues (DCt Pancreas = 18,94)

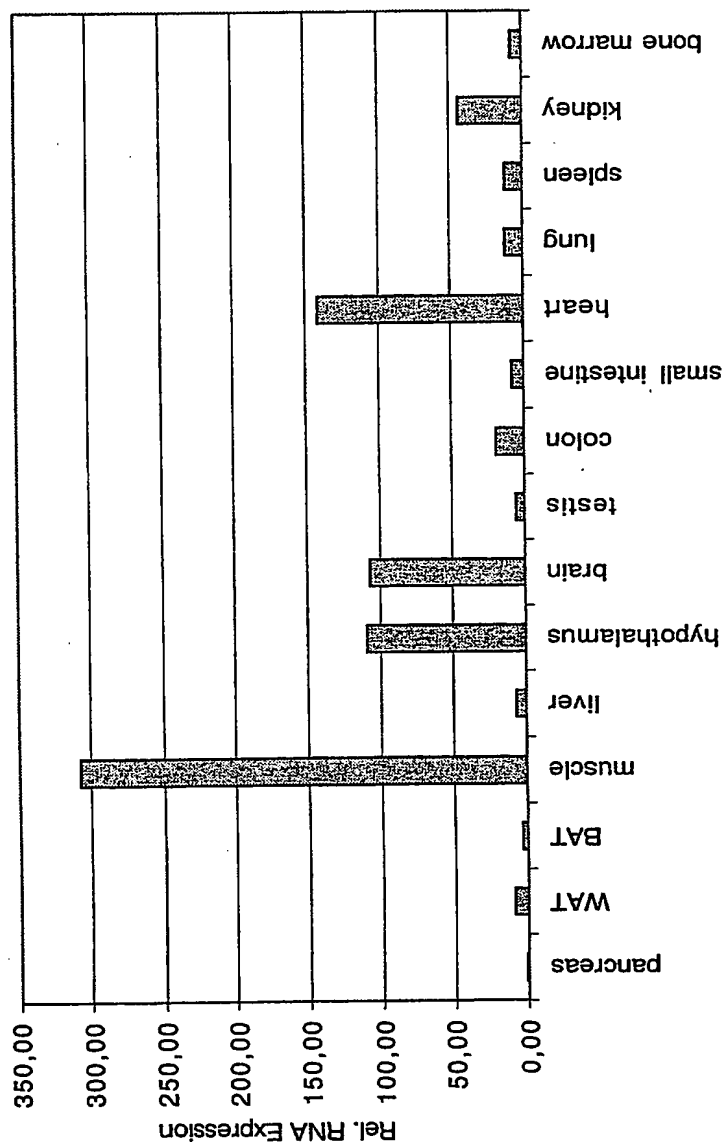


Figure 8B. Real-time PCR analysis of Slc25a12 expression in different mouse models

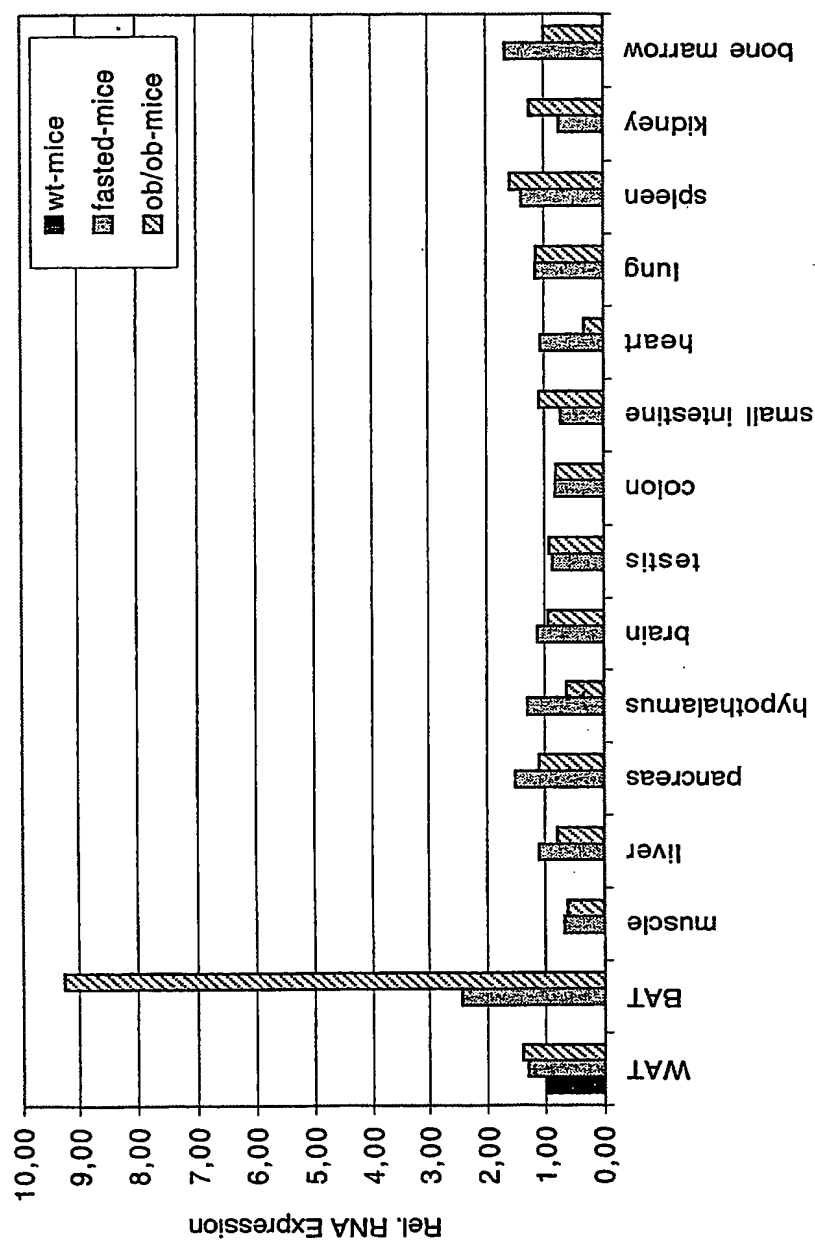


Figure 8C. Real-time PCR analysis of Slc25a13 expression in wild type mouse tissues (DCt Pancreas = 20,41)

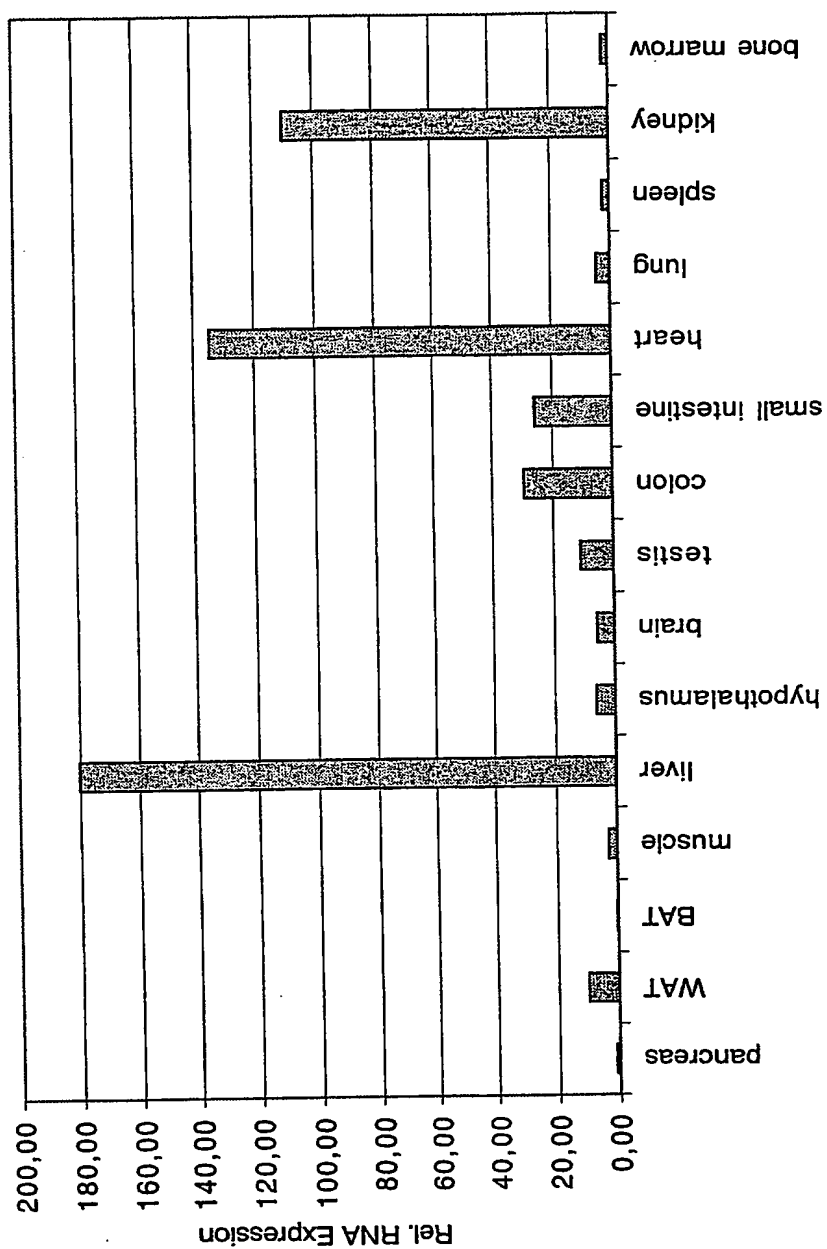


Figure 8D. Real-time PCR analysis of Slc25a13 expression in in different mouse models

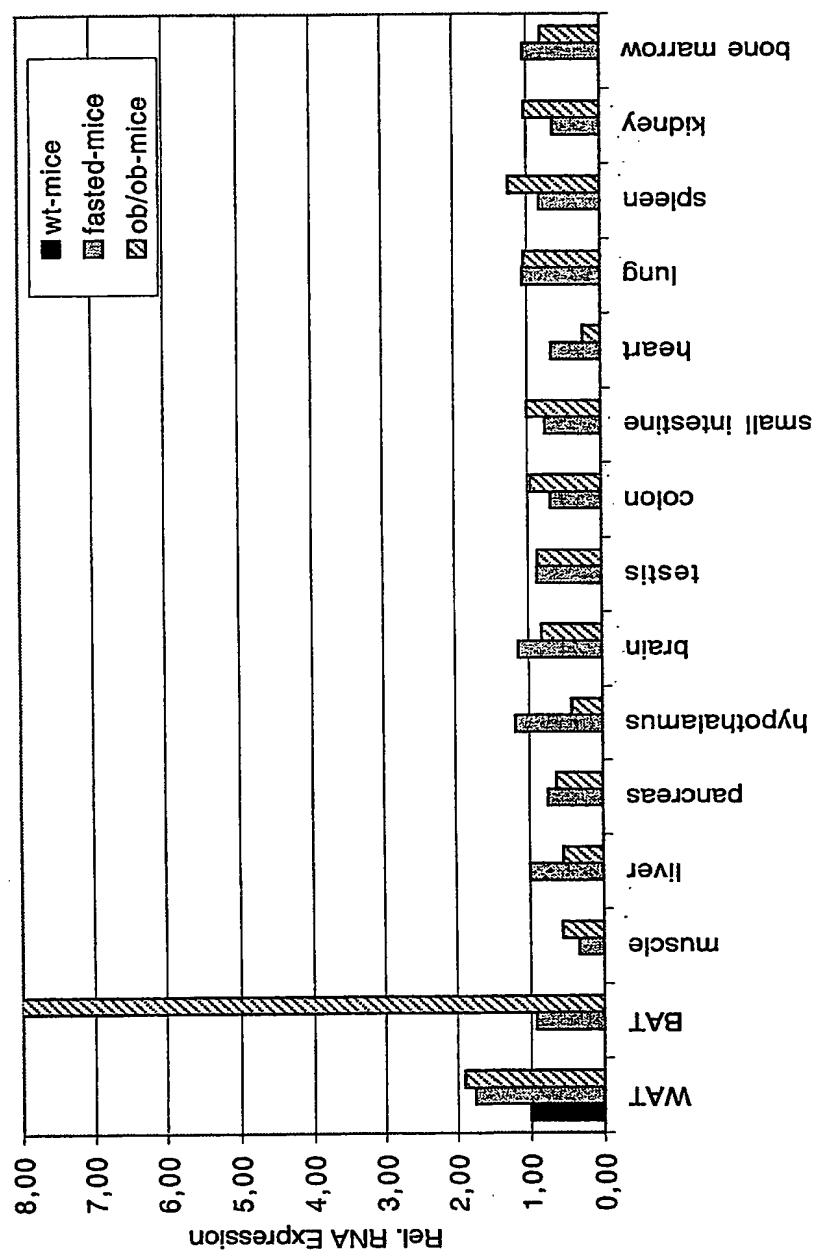


Figure 9. Triglyceride content of a *Drosophila how* (GadFly Accession Number CG10293) mutant

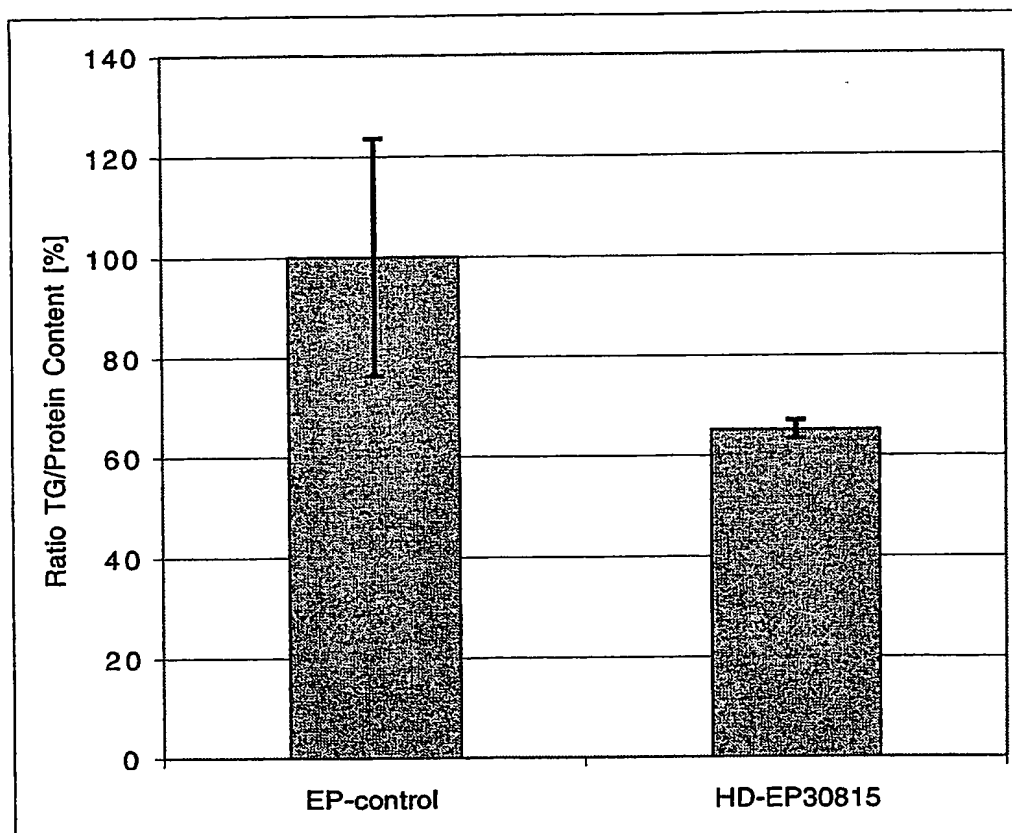


Figure 10. Molecular organisation of the *how* gene (GadFly Accession Number CG10293)

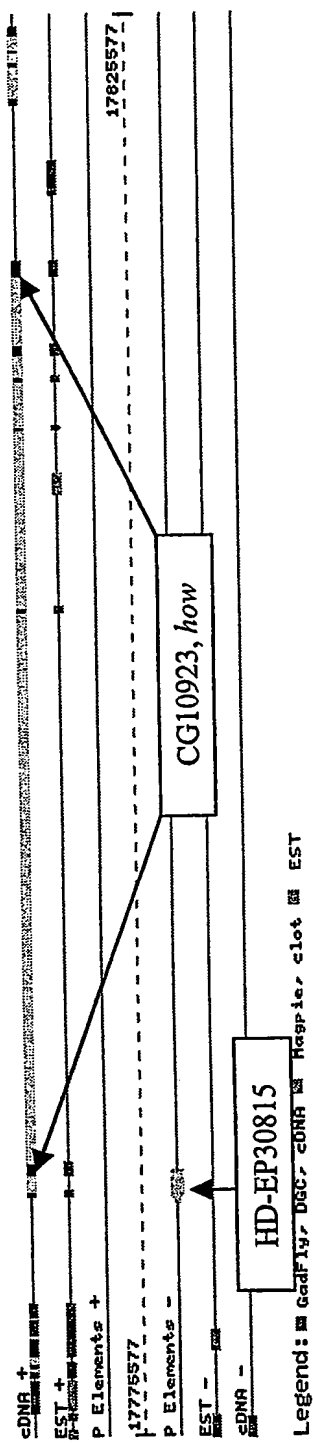


Figure 11. Homology of *Drosophila how* (GadFly Accession Number CG10293) to human Quaking isoforms

Figure 11A. BLASTP results for CG10293 (GadFly Accession Number)

gb|AAF63416.1|AF142421_1 (AF142421) QUAKING isoform 5 [Homo sapiens]
Length = 337

Score = 289 bits (739), Expect = 5e-77
Identities = 168/334 (50%), Positives = 215/334 (64%), Gaps = 20/334 (5%)

Query: 67 QQQQSTQSIADYLAQLLKDRKQLAAFPN---VFTHVERLLDEEIARVRASLFQ--ING-V 120
+ ++ + DYL QL+ D+K +++ PN +F H+ERLLDEEI+RVR ++ +NG
Sbjct: 2 ETKEKPKPTPDYLMQLMNDKKLMSSLPNFCGIFNHLERLLDEEISVRKDMYNDTLNGST 61

Query: 121 KKEPLTLPEPEGSVVTMNEKVYPVREHPDFNFVGRILGPRGMTAKQLEQETGCKIMVRG 180
+K LP+ G +V + EK+YVPV+E+PDFNFVGRILGPRG+TAKQLE ETGCKIMVRG
Sbjct: 62 EKRSAELPDAVGPIVQLQEKLYVPVKEYPDFNFVGRILGPRGLTAKQLEAETGCKIMVRG 121

Query: 181 KGSMRDKKKEDANRGKPNWEHLSDDLHVLITVEDTENRATVKLAQAVAEVQKLLVPQAEG 240
KGSMRDKKKE+ NRGKPNWEHL++DLHVLITVED +NRA +KL +AV EV+KLLVP AEG
Sbjct: 122 KGSMRDKKKKEQNRGKPNWEHLNEDLHVLITVEDAQNRAEIKLKRAVEEVKLLVPAAEG 181

Query: 241 EDELKKRQLMELAIINGTYRDTTAKSVAVCDEEWRLVAASDSRLLTSTGLPGLAAQIRA 300
ED LKK QLMELAI+NGTYRD KS A+ A + R++T A +R
Sbjct: 182 EDCLKKQLMELAILNGTYRDANIKSPALAFS--LAATAQAAPRIITGPAPVLPPAALRT 239

Query: 301 PA-AAPLGAPLILNPRMTVPTTAASILSAQAAPTAAFDQTG--HGMIFAPYDYANYAALA 357
P A P PLI + V + + PTAA G G+I+ PY+Y Y
Sbjct: 240 PTPAGPTIMPLIRQIQTAV-----MPNGTPHPTAAIVPPGPEAGLIYTPYEYP-YTLAP 292

Query: 358 GNPLLTEYADHS--VGAIKQORRLATNREHPYQR 389
+L + S +GA+ + R R HPYQR
Sbjct: 293 ATSILEYPIEPSGVLGAVATKVRHRDMRVHPYQR 326

ref|XP_037438.2| (XM_037438) similar to KH domain RNA binding protein QKI-5A
[Homo sapiens], Length = 341

Score = 289 bits (739), Expect = 5e-77
Identities = 168/334 (50%), Positives = 215/334 (64%), Gaps = 20/334 (5%)

Query: 67 QQQQSTQSIADYLAQLLKDRKQLAAFPN---VFTHVERLLDEEIARVRASLFQ--ING-V 120
+ ++ + DYL QL+ D+K +++ PN +F H+ERLLDEEI+RVR ++ +NG
Sbjct: 6 ETKEKPKPTPDYLMQLMNDKKLMSSLPNFCGIFNHLERLLDEEISVRKDMYNDTLNGST 65

Query: 121 KKEPLTLPEPEGSVVTMNEKVYPVREHPDFNFVGRILGPRGMTAKQLEQETGCKIMVRG 180
+K LP+ G +V + EK+YVPV+E+PDFNFVGRILGPRG+TAKQLE ETGCKIMVRG
Sbjct: 66 EKRSAELPDAVGPIVQLQEKLYVPVKEYPDFNFVGRILGPRGLTAKQLEAETGCKIMVRG 125

Query: 181 KGSMRDKKKEDANRGKPNWEHLSDDLHVLITVEDTENRATVKLAQAVAEVQKLLVPQAEG 240
KGSMRDKKKE+ NRGKPNWEHL++DLHVLITVED +NRA +KL +AV EV+KLLVP AEG
Sbjct: 126 KGSMRDKKKKEQNRGKPNWEHLNEDLHVLITVEDAQNRAEIKLKRAVEEVKLLVPAAEG 185

Query: 241 EDELKKRQLMELAIINGTYRDTTAKSVAVCDEEWRLVAASDSRLLTSTGLPGLAAQIRA 300
ED LKK QLMELAI+NGTYRD KS A+ A + R++T A +R
Sbjct: 186 EDCLKKQLMELAILNGTYRDANIKSPALAFS--LAATAQAAPRIITGPAPVLPPAALRT 243

19/51

Query: 301 PA-AAPLGAPLILNPRMTVPTTAASILSAQAAPTAAFDQTG--HGMIFAPYDYANYAALA 357
P A P PLI + V + + PTAA G G+I+ PY+Y Y
Sbjct: 244 PTPAGPTIMPLIRQIQTA-----MPNGTPHPTAAIVPPGPEAGLIYTPYEYP-YTLAP 296

Query: 358 GNPLLTEYADHS--VGAIKQORRLATNREHPYQR 389
+L + S +GA+ + R R HPYQR
Sbjct: 297 ATSILEYPIEPSGVLGAVATKVRRHDMRVHPYQR 330

gb|AAF63414.1|AF142419_1 (AF142419) QUAKING isoform 6 [Homo sapiens]
Length = 363

Score = 289 bits (739), Expect = 5e-77
Identities = 168/334 (50%), Positives = 215/334 (64%), Gaps = 20/334 (5%)

Query: 67 QQQQSTQSIADYLAQLLKDRKQLAAFPN---VFTHVERLLDEEIARVRASLFQ--ING-V 120
+ ++ + DYL QL+ D+K +++ PN +F H+ERLLDEEI+RVR ++ +NG
Sbjct: 28 ETKEKPKPTPDYLMQLMNDKKLMSSLPNFCGIFNHLERLLDEEISVRKDMYNDTLNGST 87

Query: 121 KKEPLTLPEPEGSVVTMNEKVYPVREHPDFNFVGRILGPRGMTAKQLEQETGCKIMVRG 180
+K LP+ G +V + EK+YVPV+E+PDFNFVGRILGPRG+TAKQLE ETGCKIMVRG
Sbjct: 88 EKRSAELPDAVGPIVQLQEKLYVPVKEYPDFNFVGRILGPRGLTAKQLEAETGCKIMVRG 147

Query: 181 KGSMRDKKKEDANRGKPNWEHLSDDLHVLITVEDTENRATVKLAQAVAEVQKLLVPAEG 240
KGSMRDKKKE+ NRGKPNWEHL++DLHVLITVED +NRA +KL +AV EV+KLLVP AEG
Sbjct: 148 KGSMRDKKKEEQNRGKPNWEHLNEDLHVLITVEDAQNRAEIKLKRAVEEVKLLVPAEG 207

Query: 241 EDELKKRQLMELAIINGTYRDTTAKSVAVCDEEWRLVAASDSRLLTSTGLPGLAAQIRA 300
ED LKK QLMELAI+NGTYRD KS A+ A + R++T A +R
Sbjct: 208 EDSLKKMQLMELAILNGTYRDANIKSPALAFS--LAATAQAAPRIITGPAPVLPAPALRT 265

Query: 301 PA-AAPLGAPLILNPRMTVPTTAASILSAQAAPTAAFDQTG--HGMIFAPYDYANYAALA 357
P A P PLI + V + + PTAA G G+I+ PY+Y Y
Sbjct: 266 PTPAGPTIMPLIRQIQTA-----MPNGTPHPTAAIVPPGPEAGLIYTPYEYP-YTLAP 318

Query: 358 GNPLLTEYADHS--VGAIKQORRLATNREHPYQR 389
+L + S +GA+ + R R HPYQR
Sbjct: 319 ATSILEYPIEPSGVLGAVATKVRRHDMRVHPYQR 352

dbj|BAB55032.1| (AK027309) unnamed protein product [Homo sapiens]
Length = 323

Score = 282 bits (722), Expect = 5e-75
Identities = 165/320 (51%), Positives = 208/320 (64%), Gaps = 20/320 (6%)

Query: 81 QLLKDRKQLAAFPN---VFTHVERLLDEEIARVRASLFQ--ING-VKKEPLTLPEPEGSV 134
QL+ D+K +++ PN +F H+ERLLDEEI+RVR ++ +NG +K LP+ G +
Sbjct: 2 QLMNDKKLMSSLPNFCGIFNHLERLLDEEISVRKDMYNDTLNGSTEKRSAELPDAVGPI 61

Query: 135 VTMNEKVYPVREHPDFNFVGRILGPRGMTAKQLEQETGCKIMVRGKGSMRDKKKEDANR 194
V + EK+YVPV+E+PDFNFVGRILGPRG+TAKQLE ETGCKIMVRGKGSMRDKKKE+ NR
Sbjct: 62 VQLQEKLYVPVKEYPDFNFVGRILGPRGLTAKQLEAETGCKIMVRGKGSMRDKKKEQNR 121

Query: 195 GKPNWEHLSDDLHVLITVEDTENRATVKLAQAVAEVQKLLVPAEGEDELKKRQLMELAI 254
GKPNWEHL++DLHVLITVED +NRA +KL +AV EV+KLLVP AEGED LKK QLMELAI
Sbjct: 122 GKPNWEHLNEDLHVLITVEDAQNRAEIKLKRAVEEVKLLVPAEAGEDSLKKMQLMELAI 181

Query: 255 INGTYRDTTAKSVAVCDEEWRLVAASDSRLLTSTGLPGLAAQIRAPA-AAPLGAPLILN 313
+NGTYRD KS A+ A + R++T A +R P A P PLI
Sbjct: 182 LNGTYRDANIKSPALAFS--LAATAQAAPRIITGPAPVLPAPALRTPTPAGPTIMPLIRQ 239

Query: 314 PRMTVPTTAASILSAQAAPTAAFDQTG--HGMIFAPYDYANYAALAGNPLLTEYADHS-- 369
+ V + + PTAA G G+I+ PY+Y Y +L + S
Sbjct: 240 IQTAV-----MPNGTPHPTAAIVPPGPEAGLIYTPYEYP-YTLAPATSILEYPIEPSGV 292

Query: 370 VGAIKQORRLATNREHPYQR 389
+GA+ + R R HPYQR
Sbjct: 293 LGAVATKVRRHDMRVHPYQR 312

gb|AAF63413.1|AF142418_1 (AF142418) QUAKING isoform 2 [Homo sapiens]
Length = 347

Score = 280 bits (716), Expect = 2e-74
Identities = 156/293 (53%), Positives = 198/293 (67%), Gaps = 17/293 (5%)

Query: 67 QQQQSTQSIADYLAQLLKDRKQLAAFPN---VFTHVERLLDEEIIARVRASLFQ--ING-V 120
+ ++ + DYL QL+ D+K +++ PN +F H+ERLLDEEI+RVR ++ +NG
Sbjct: 28 ETKEKPKPTPDYLMQMLMNDKKLMSSLPNFCGIFNHLERLLDEEISVRKMDMYNDTLNGST 87

Query: 121 KKEPLTLPEPEGSVVTMNEKVYPVREHPDFNFVGRILGPRGMTAKQLEQETGCKIMVRG 180
+K LP+ G +V + EK+YVPV+E+PDFNFVGRILGPRG+TAKQLE ETGCKIMVRG
Sbjct: 88 EKRSAELPDAVGPIVQLQEKLYVPVKEYPDFNFVGRILGPRGLTAKQLEAETGCKIMVRG 147

Query: 181 KGSMRDKKKEDANRGKPNWEHLSDDLHVLITVEDTENRATVKLAQAVAEOVKLLVPQAEG 240
KGSMRDKKKE+ NRGKPNWEHL++DLHVLITVED +NRA +KL +AV EV+KLLVP AEG
Sbjct: 148 KGSMRDKKKEEQNRGKPNWEHLNEDLHVLITVEDAQNRAEIKLKRAVEEVKLLVPAAEG 207

Query: 241 EDELKKRQLMELAIINGTYRDTTAKSVAVCDEEWRLVAASDSRLLTSTGLPGLAAQIRA 300
ED LKK QLMELAI+NGTYRD KS A+ A + R++T A +R
Sbjct: 208 EDSLKKMQLMELAILNGTYRDANIKSPALAFS--LAATAQAAPRIITGPAPVLPAPALRT 265

Query: 301 PA-AAPLGAPLILNPRMTVPTTAASILSAQAAPTAAFDQTG--HGMIFAPYDY 350
P A P PLI + V + + PTAA G G+I+ PY+Y
Sbjct: 266 PTPAGPTIMPLIRQIQTAV-----MPNGTPHPTAAIVPPGPEAGLIYTPYEY 312

gb|AAF63417.1|AF142422_1 (AF142422) QUAKING isoform 3 [Homo sapiens]
Length = 341

Score = 280 bits (716), Expect = 2e-74
Identities = 156/293 (53%), Positives = 198/293 (67%), Gaps = 17/293 (5%)

Query: 67 QQQQSTQSIADYLAQLLKDRKQLAAFPN---VFTHVERLLDEEIIARVRASLFQ--ING-V 120
+ ++ + DYL QL+ D+K +++ PN +F H+ERLLDEEI+RVR ++ +NG
Sbjct: 28 ETKEKPKPTPDYLMQMLMNDKKLMSSLPNFCGIFNHLERLLDEEISVRKMDMYNDTLNGST 87

Query: 121 KKEPLTLPEPEGSVVTMNEKVYPVREHPDFNFVGRILGPRGMTAKQLEQETGCKIMVRG 180
+K LP+ G +V + EK+YVPV+E+PDFNFVGRILGPRG+TAKQLE ETGCKIMVRG
Sbjct: 88 EKRSAELPDAVGPIVQLQEKLYVPVKEYPDFNFVGRILGPRGLTAKQLEAETGCKIMVRG 147

Query: 181 KGSMRDKKKEDANRGKPNWEHLSDDLHVLITVEDTENRATVKLAQAVAEOVKLLVPQAEG 240
KGSMRDKKKE+ NRGKPNWEHL++DLHVLITVED +NRA +KL +AV EV+KLLVP AEG
Sbjct: 148 KGSMRDKKKEEQNRGKPNWEHLNEDLHVLITVEDAQNRAEIKLKRAVEEVKLLVPAAEG 207

Query: 241 EDELKKRQLMELAIINGTYRDTTAKSVAVCDEEWRLVAASDSRLLTSTGLPGLAAQIRA 300
 ED LKK QLMELAI+NGTYRD KS A+ A + R++T A +R
 Sbjct: 208 EDSLKKMQLMELAILNGTYRDANIKSPALAFS--LAATAQAAPRIITGPAPVLPAAALRT 265

Query: 301 PA-AAPLGAPLILNPRMTVPTTAASILSAQAAPTAAFDQTG--HGMIFAPYDY 350
 P A P PLI + V + + PTAA G G+I+ PY+Y
 Sbjct: 266 PTPAGPTIMPLIRIQITAV-----MPNGTPHPTAAIVPPGPEAGLIYTPYDY 312

gb|AAF63415.1|AF142420_1 (AF142420) QUAKING isoform 4 [Homo sapiens]
 Length = 315

Score = 280 bits (716), Expect = 2e-74
 Identities = 156/293 (53%), Positives = 198/293 (67%), Gaps = 17/293 (5%)

Query: 67 QQQQSTQSIADYLAQLLKDRKQLAAFPN---VFTHVERLLDEEIARVRASLFQ--ING-V 120
 + ++ + DYL QL+ D+K +++ PN +F H+ERLLDEEI+RVR ++ +NG
 Sbjct: 2 ETKEKPKPTPDYLMQLMNDKKLMSSLPNFCGIFNHLERLLDEEISRVRKDMYNDTLNGST 61

Query: 121 KKEPLTLPEPEGSVVTMNEKVYVPVREHPDFNFVGRILGPRGMTAKQLEQETGCKIMVRG 180
 +K LP+ G +V + EK+YVPV+E+PDFNFVGRILGPRG+TAKQLE ETGCKIMVRG
 Sbjct: 62 EKRSAELPDAVGPIVQLQEKLYVPVKEYPDFNFVGRILGPRGLTAKQLEAETGCKIMVRG 121

Query: 181 KGSMRDKKKEDANRGKPNWEHLSDDLHVLITVEDTENRATVKLAQAVAQVQKLLVPQAEG 240
 KGSMRDKKKE+ NRGKPNWEHL++DLHVLITVED +NRA +KL +AV EV+KLLVP AEG
 Sbjct: 122 KGSMRDKKKEQNRGKPNWEHLNEDLHVLITVEDAQNRAEIKLKRAVEEVKLLVPAAEG 181

Query: 241 EDELKKRQLMELAIINGTYRDTTAKSVAVCDEEWRLVAASDSRLLTSTGLPGLAAQIRA 300
 ED LKK QLMELAI+NGTYRD KS A+ A + R++T A +R
 Sbjct: 182 EDSLKKMQLMELAILNGTYRDANIKSPALAFS--LAATAQAAPRIITGPAPVLPAAALRT 239

Query: 301 PA-AAPLGAPLILNPRMTVPTTAASILSAQAAPTAAFDQTG--HGMIFAPYDY 350
 P A P PLI + V + + PTAA G G+I+ PY+Y
 Sbjct: 240 PTPAGPTIMPLIRIQITAV-----MPNGTPHPTAAIVPPGPEAGLIYTPYDY 286

dbj|BAB69497.1| (AB067799) RNA binding protein HQK-6 [Homo sapiens]
 Length = 319

Score = 280 bits (716), Expect = 2e-74
 Identities = 156/293 (53%), Positives = 198/293 (67%), Gaps = 17/293 (5%)

Query: 67 QQQQSTQSIADYLAQLLKDRKQLAAFPN---VFTHVERLLDEEIARVRASLFQ--ING-V 120
 + ++ + DYL QL+ D+K +++ PN +F H+ERLLDEEI+RVR ++ +NG
 Sbjct: 6 ETKEKPKPTPDYLMQLMNDKKLMSSLPNFCGIFNHLERLLDEEISRVRKDMYNDTLNGST 65

Query: 121 KKEPLTLPEPEGSVVTMNEKVYVPVREHPDFNFVGRILGPRGMTAKQLEQETGCKIMVRG 180
 +K LP+ G +V + EK+YVPV+E+PDFNFVGRILGPRG+TAKQLE ETGCKIMVRG
 Sbjct: 66 EKRSAELPDAVGPIVQLQEKLYVPVKEYPDFNFVGRILGPRGLTAKQLEAETGCKIMVRG 125

Query: 181 KGSMRDKKKEDANRGKPNWEHLSDDLHVLITVEDTENRATVKLAQAVAQVQKLLVPQAEG 240
 KGSMRDKKKE+ NRGKPNWEHL++DLHVLITVED +NRA +KL +AV EV+KLLVP AEG
 Sbjct: 126 KGSMRDKKKEQNRGKPNWEHLNEDLHVLITVEDAQNRAEIKLKRAVEEVKLLVPAAEG 185

Query: 241 EDELKKRQLMELAIINGTYRDTTAKSVAVCDEEWRLVAASDSRLLTSTGLPGLAAQIRA 300
 ED LKK QLMELAI+NGTYRD KS A+ A + R++T A +R
 Sbjct: 186 EDSLKKMQLMELAILNGTYRDANIKSPALAFS--LAATAQAAPRIITGPAPVLPAAALRT 243

Query: 301 PA-AAPLGAPLILNPRMTVPTTAASILSAQAAPTAAFDQTG--HGMIFAPYDY 350
 P A P PLI + V + + PTAA G G+I+ PY+Y
 Sbjct: 244 PTPAGPTIMPLIRQIQTAV-----MPNGTPHPTAAIVPPGPEAGLIYTPYEY 290

dbj|BAB69499.1| (AB067801) RNA binding protein HQK-7B [Homo sapiens]
 Length = 319

Score = 280 bits (716), Expect = 2e-74
 Identities = 156/293 (53%), Positives = 198/293 (67%), Gaps = 17/293 (5%)

Query: 67 QQQQSTQSIADYLAQLLKDRKQLAAFPN---VFTHVERLLDEEIARVRASLFQ--ING-V 120
 + ++ + DYL QL+ D+K +++ PN +F H+ERLLDEEI+RVR ++ +NG
 Sbjct: 6 ETKEKPKPTPDYLMQLMNDKKLMSSLPNFCGIFNHLERLLDEEISVRKDMYNDTLNGST 65

Query: 121 KKEPLTLPEPEGSVVTMNEKVYVPVREHPDFNFVGRILGPRGMTAKQLEQETGCKIMVRG 180
 +K LP+ G +V + EK+YVPV+E+PDFNFVGRILGPRG+TAKQLE ETGCKIMVRG
 Sbjct: 66 EKRSAELPDAVGPIVQLQEKLYVPVKEYPDFNFVGRILGPRGLTAKQLEAETGCKIMVRG 125

Query: 181 KGSMRDKKKEDANRGKPNWEHLSDDLHVLITVEDTENRATVKLAQAVAEVQKLLVPPQAEG 240
 KGSMRDKKKE+ NRGKPNWEHL++DLHVLITVED +NRA +KL +AV EV+KLLVP AEG
 Sbjct: 126 KGSMRDKKKKEQNRGKPNWEHLNEDLHVLITVEDAQNRAEIKLKRAVEEVKLLVPAAEG 185

Query: 241 EDELKKRQLMELAIINGTYRDTTAKSVAVCDEEWRLVAASDSRLLTSTGLPGLAAQIRA 300
 ED LKK QLMELAI+NGTYRD KS A+ A + R++T A +R
 Sbjct: 186 EDCLKKMQLMELAILNGTYRDANIKSPALAFS--LAATAQAAPRIITGPAPVLPPAALRT 243

Query: 301 PA-AAPLGAPLILNPRMTVPTTAASILSAQAAPTAAFDQTG--HGMIFAPYDY 350
 P A P PLI + V + + PTAA G G+I+ PY+Y
 Sbjct: 244 PTPAGPTIMPLIRQIQTAV-----MPNGTPHPTAAIVPPGPEAGLIYTPYEY 290

dbj|BAB69498.1| (AB067800) RNA binding protein HQK-7 [Homo sapiens]
 Length = 325

Score = 280 bits (716), Expect = 2e-74
 Identities = 156/293 (53%), Positives = 198/293 (67%), Gaps = 17/293 (5%)

Query: 67 QQQQSTQSIADYLAQLLKDRKQLAAFPN---VFTHVERLLDEEIARVRASLFQ--ING-V 120
 + ++ + DYL QL+ D+K +++ PN +F H+ERLLDEEI+RVR ++ +NG
 Sbjct: 6 ETKEKPKPTPDYLMQLMNDKKLMSSLPNFCGIFNHLERLLDEEISVRKDMYNDTLNGST 65

Query: 121 KKEPLTLPEPEGSVVTMNEKVYVPVREHPDFNFVGRILGPRGMTAKQLEQETGCKIMVRG 180
 +K LP+ G +V + EK+YVPV+E+PDFNFVGRILGPRG+TAKQLE ETGCKIMVRG
 Sbjct: 66 EKRSAELPDAVGPIVQLQEKLYVPVKEYPDFNFVGRILGPRGLTAKQLEAETGCKIMVRG 125

Query: 181 KGSMRDKKKEDANRGKPNWEHLSDDLHVLITVEDTENRATVKLAQAVAEVQKLLVPPQAEG 240
 KGSMRDKKKE+ NRGKPNWEHL++DLHVLITVED +NRA +KL +AV EV+KLLVP AEG
 Sbjct: 126 KGSMRDKKKKEQNRGKPNWEHLNEDLHVLITVEDAQNRAEIKLKRAVEEVKLLVPAAEG 185

Query: 241 EDELKKRQLMELAIINGTYRDTTAKSVAVCDEEWRLVAASDSRLLTSTGLPGLAAQIRA 300
 ED LKK QLMELAI+NGTYRD KS A+ A + R++T A +R
 Sbjct: 186 EDCLKKMQLMELAILNGTYRDANIKSPALAFS--LAATAQAAPRIITGPAPVLPPAALRT 243

Query: 301 PA-AAPLGAPLILNPRMTVPTTAASILSAQAAPTAAFDQTG--HGMIFAPYDY 350
 P A P PLI + V + + PTAA G G+I+ PY+Y
 Sbjct: 244 PTPAGPTIMPLIRQIQTAV-----MPNGTPHPTAAIVPPGPEAGLIYTPYEY 290

gb|AAF63412.1|AF142417_1 (AF142417) QUAKING isoform 1 [Homo sapiens]
Length = 321

Score = 280 bits (716), Expect = 2e-74
Identities = 156/293 (53%), Positives = 198/293 (67%), Gaps = 17/293 (5%)

Query: 67 QQQQSTQSIADYLAQLLKDRKQLAAFPN---VFTHVERLLDEEIIARVRASLFQ--ING-V 120
+ ++ + DYL QL+ D+K +++ PN +F H+ERLLDEEII+RVR ++ +NG
Sbjct: 2 ETKEKPKPTPDYLMQLMNDKKLMSSLPNFCGIFNHLERLLDEEISRVKMDMYNDTLNGST 61

Query: 121 KKEPLTLPEPEGSVVTMNEKVYPVREHPDFNFVGRILGPRGMTAKQLEQETGCKIMVRG 180
+K LP+ G +V + EK+YVPV+E+PDFNFVGRILGPRG+TAKQLE ETGCKIMVRG
Sbjct: 62 EKRSAELPDVGPVQLQEKLYVPVKEYPDFNFVGRILGPRGLTAKQLEAETGCKIMVRG 121

Query: 181 KGSMRDKKKEDANRGKPNWEHLSDDLHVLITVEDTENRATVKLAQAVAEVQKLLVPQAEG 240
KGSMRDKKKE+ NRGKPNWEHL++DLHVLITVED +NRA +KL +AV EV+KLLVP AEG
Sbjct: 122 KGSMRDKKKEEQNRGKPNWEHLNEDLHVLITVEDAQNRAEIKLKRAVEEVKLLVPAAEG 181

Query: 241 EDELKKRQLMELAIINGTYRDTTAKSVAVCDEEWRLVAASDSRLLTSTGLPGLAAQIRA 300
ED LKK QLMELAI+NGTYRD KS A+ A + R++T A +R
Sbjct: 182 EDCLKKQLMELAILNGTYRDANIKSPALAFS--LAATAQAAPRIITGPAPVLPALRT 239

Query: 301 PA-AAPLGAPLILNPRMTVPTTAASILSAQAAPTAAFDQTG--HGMIFAPYDY 350
P A P PLI + V + + PTAA G G+I+ PY+Y
Sbjct: 240 PTPAGPTIMPLIRIQITAV-----MPNGTPHPTAAIVPPGPEAGLIYTPYEY 286

dbj|BD004960.1| Genes related to stomach cancer, Length = 1993

Score = 288 bits (738), Expect = 1e-77
Identities = 168/324 (51%), Positives = 211/324 (64%), Gaps = 11/324 (3%)
Frame = +1

Query: 77 DYLAQLLKDRKQLAAFPN---VFTHVERLLDEEIIARVRASLFQ--ING-VKKEPLTLPEP 130
DYL QL+ D+K +++ PN +F H+ERLLDEEII+RVR ++ +NG +K LP+
Sbjct: 4 DYLMQLMNDKKLMSSLPNFCGIFNHLERLLDEEISRVKMDMYNDTLNGSTEKRSALPD 183

Query: 131 EGSVVTMNEKVYPVREHPDFNFVGRILGPRGMTAKQLEQETGCKIMVRGKGSMRDKKKE 190
G +V + EK+YVPV+E+PDFNFVGRILGPRG+TAKQLE ETGCKIMVRGKGSMRDKKKE
Sbjct: 184 VGPIVQLQEKLYVPVKEYPDFNFVGRILGPRGLTAKQLEAETGCKIMVRGKGSMRDKKKE 363

Query: 191 DANRGKPNWEHLSDDLHVLITVEDTENRATVKLAQAVAEVQKLLVPQAEGEDELKKRQLM 250
+ NRGKPNWEHL++DLHVLITVED +NRA +KL +AV EV+KLLVP AEGED LKK QLM
Sbjct: 364 EQNRGKPNWEHLNEDLHVLITVEDAQNRAEIKLKRAVEEVKLLVPAAEGEDSLKMQLM 543

Query: 251 ELAIINGTYRDTTAKSVAVCDEEWRLVAASDSRLLTSTGLPGLAAQIRAPA-AAPLGAP 309
ELAI+NGTYRD KS A+ A + R++T A +R P A P P
Sbjct: 544 ELAILNGTYRDANIKSPALAFS--LAATAQAAPRIITGPAPVLPALRTPTPAGPTIMP 717

Query: 310 LILNPRMTVPTTAASILSAQAAPTAAFDQTG--HGMIFAPYDYANYAALAGNPLLTEYAD 367
LI + V + + PTAA G G+I+ PY+Y Y +L +
Sbjct: 718 LIRIQITAV-----MPNGTPHPTAAIVPPGPEAGLIYTPYEY-YTLAPATSILEYPIE 876

Query: 368 HS--VGAIKQORRLATNREHPYQR 389
S +GA+ + R R HPYQR
Sbjct: 877 PSGVLGAVATKVRRHDMRVHPYQR

CG10293 Dm MSVCESKAVVQQQLQQHLQQQAAAAVVAQQQQAAQAQAQAQAQQQQQAPQVVVPMPT
QKI-6 Hs -----MLSLSSLRRNSGRNSGSCGAWN-----
QKI-2 Hs -----MLSLSSLRRNSGRNSGSCGAWN-----
QKI-3 Hs -----MLSLSSLRRNSGRNSGSCGAWN-----
HQK-7B Hs -----

CG10293 Dm QHLTPQQQQQSTQSIADYLAQLLKDRKQLAAFPN---VFTHVERLLDEEIARVRASLF--
QKI-6 Hs -MVGEMETKEKPKPTPDYLMQLMNDKKLMSSLPNFCGIFNHLERLLDEEISRVRKDMYND
QKI-2 Hs -MVGEMETKEKPKPTPDYLMQLMNDKKLMSSLPNFCGIFNHLERLLDEEISRVRKDMYND
QKI-3 Hs -MVGEMETKEKPKPTPDYLMQLMNDKKLMSSLPNFCGIFNHLERLLDEEISRVRKDMYND
HQK-7B Hs -MVGEMETKEKPKPTPDYLMQLMNDKKLMSSLPNFCGIFNHLERLLDEEISRVRKDMYND

CG10293 Dm QING-VKKEPLTLPEPEGSVVTMNEKVYVPVREHPDFNFVGRILGPRGMTAKQLEQETGC
QKI-6 Hs TLNGSTEKRSaelPDAVGPIVQLQEKLYVPVKEYPDFNFVGRILGPRGLTAKQLEAETGC
QKI-2 Hs TLNGSTEKRSaelPDAVGPIVQLQEKLYVPVKEYPDFNFVGRILGPRGLTAKQLEAETGC
QKI-3 Hs TLNGSTEKRSaelPDAVGPIVQLQEKLYVPVKEYPDFNFVGRILGPRGLTAKQLEAETGC
HQK-7B Hs TLNGSTEKRSaelPDAVGPIVQLQEKLYVPVKEYPDFNFVGRILGPRGLTAKQLEAETGC

CG10293 Dm KIMVRGKGSMDKKKEDANRGKPNWEHLSDDLHLVITVEDTENRATVKLAQAVAeVQKLL
QKI-6 Hs KIMVRGKGSMDKKKEEQNRGKPNWEHLNEDLHLVITVEDAQNRaeIKLKRAVEEVKLL
QKI-2 Hs KIMVRGKGSMDKKKEEQNRGKPNWEHLNEDLHLVITVEDAQNRaeIKLKRAVEEVKLL
QKI-3 Hs KIMVRGKGSMDKKKEEQNRGKPNWEHLNEDLHLVITVEDAQNRaeIKLKRAVEEVKLL
HQK-7B Hs KIMVRGKGSMDKKKEEQNRGKPNWEHLNEDLHLVITVEDAQNRaeIKLKRAVEEVKLL

CG10293 Dm VPQAEGEDELKKRQLMELAIINGTYRDTTAKSVAVCDEEWRLVAASDSRLITSTGLPGL
QKI-6 Hs VPAAEGEDSLKKMQLMELAILNGTYRDANIKSPALAFSLAATAQAAP--RIITGPAPVLP
QKI-2 Hs VPAAEGEDSLKKMQLMELAILNGTYRDANIKSPALAFSLAATAQAAP--RIITGPAPVLP
QKI-3 Hs VPAAEGEDSLKKMQLMELAILNGTYRDANIKSPALAFSLAATAQAAP--RIITGPAPVLP
HQK-7B Hs VPAAEGEDSLKKMQLMELAILNGTYRDANIKSPALAFSLAATAQAAP--RIITGPAPVLP

CG10293 Dm AAQIRAP-AAAPLGAPLILNPRMTVPTTAASILSAQAAPTAAFDQTG--HGMIFAPYDYA
QKI-6 Hs PAALRTPTPAGPTIMPLIR-----QIQTAVMNGTPhPTAAIVPPGPEAGLIYTPYEYP
QKI-2 Hs PAALRTPTPAGPTIMPLIR-----QIQTAVMNGTPhPTAAIVPPGPEAGLIYTPYEYP
QKI-3 Hs PAALRTPTPAGPTIMPLIR-----QIQTAVMNGTPhPTAAIVPPGPEAGLIYTPYEYP
HQK-7B Hs PAALRTPTPAGPTIMPLIR-----QIQTAVMNGTPhPTAAIVPPGPEAGLIYTPYEYP

CG10293 Dm NYAALAGNPLLTEYADHSVGAIKQORRLATNREHPYQRATVGVPAKPAGFIEIQ
QKI-6 Hs --YTLAPATSILEYPIEPSGVLGAVATKVRHDMRVHPYQRIVTADRAATGN--
QKI-2 Hs --YTLAPATSILEYPIEPSGVLGMAFPPTKG-----
QKI-3 Hs --YTLAPATSILEYPIEPSGVLGMAFPPTKG-----
HQK-7B Hs --YTLAPATSILEYPIEPSGVLGKFFSPWG-----

Figure 12. Expression of human *low* homologs in mammalian (human) tissue

Figure 12A. Quantitative analysis of Quaking 6 (QKI-6) expression in human abdominal adipocyte cells during the differentiation from preadipocytes to mature adipocytes

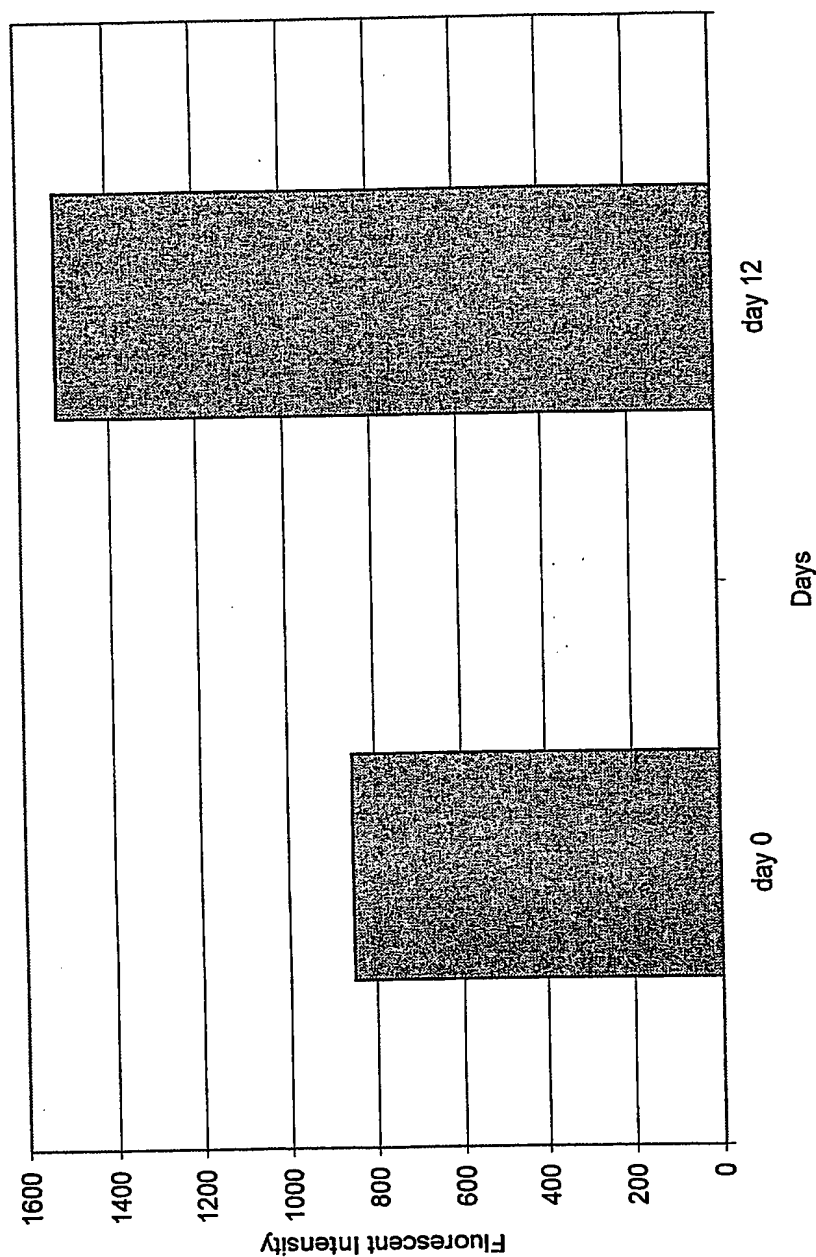


Figure 12B. Quantitative analysis of human RNA binding protein HQK-7B expression in human abdominal adipocyte cells during the differentiation from preadipocytes to mature adipocytes

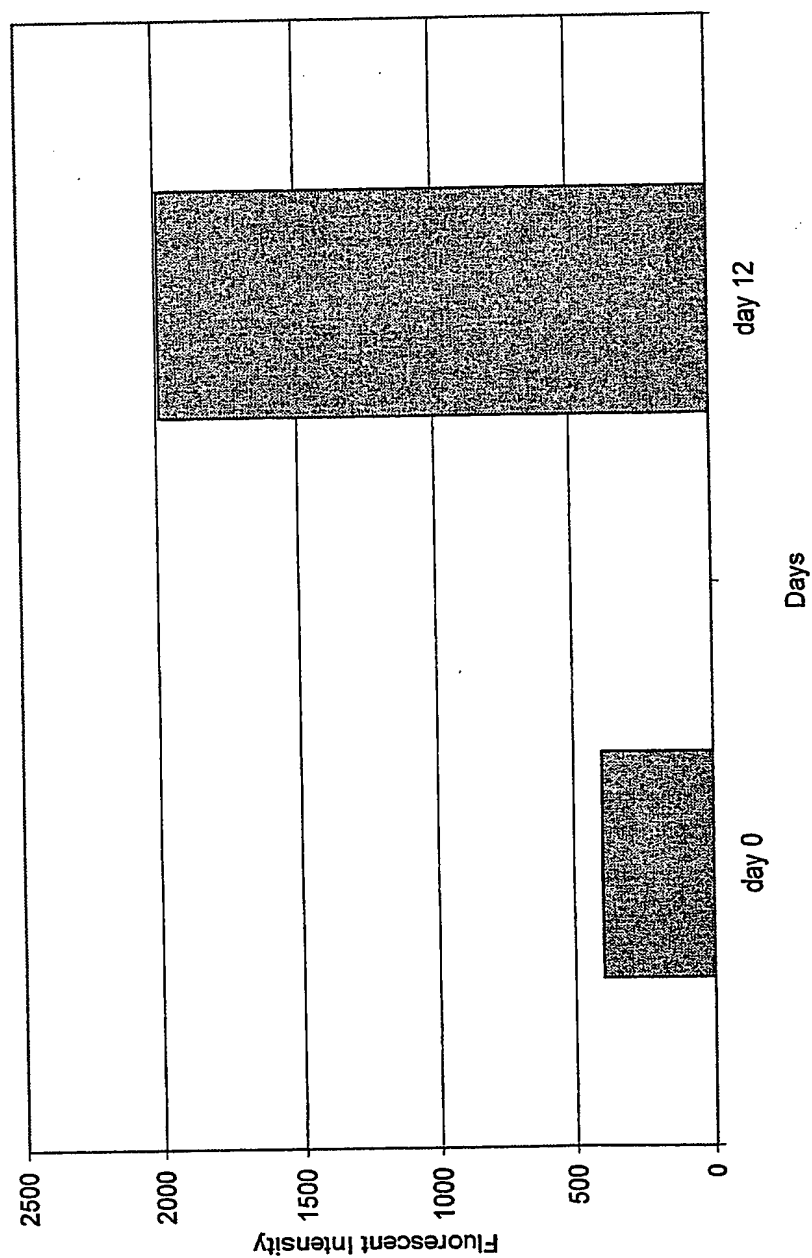


Figure 13. Triglyceride content of a *Drosophila* CG9373 (GadFly Accession Number) mutant

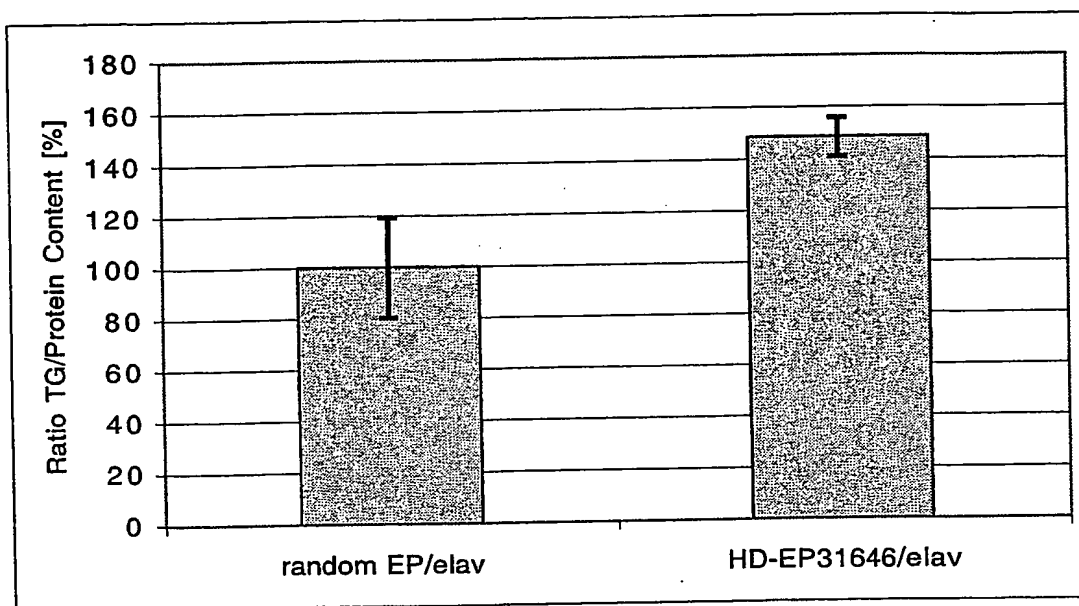


Figure 14. Molecular organisation of the CG9373 gene (GadFly Accession Number)

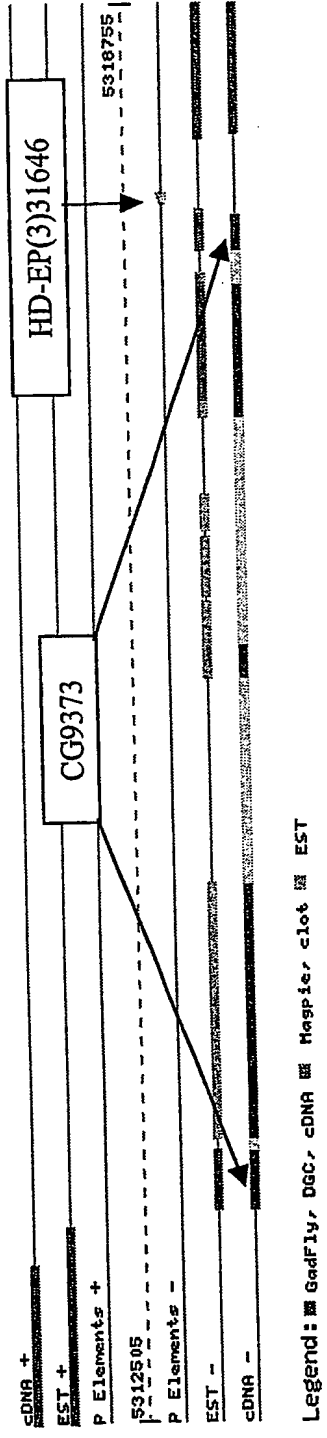


Figure 15. Homology of Drosopila GadFly Accession Number CG9373 to human KIAA1443 protein, human unnamed protein product, and human myelin gene expression factor 2

**Figure 15A. BLASTP results for GadFly Accession Number CG9373
Homology to human protein BAA92579.1 (GenBank Accession Number)**

dbj|BAA92579.1| (AB037762) KIAA1341 protein [Homo sapiens], Length = 620

Score = 249 bits (635), Expect = 1e-64

Identities = 207/660 (31%), Positives = 295/660 (44%), Gaps = 148/660 (22%)

```

Query: 1  MSMDASNSVESREKERDRRGRGAR-GSRFTDADGNGN-GAGSQGGGVAARDRSRERRNCR 58
      + M+  S + + + + G++ +RF      + N G G + G      RN R
Sbjct: 72  VKMENDESAKEEKSDLKEKSTGSKKANRFHPYSKDKNSGTGEKKG-----PNRN-R 121

Query: 59  VYISNIPYDYRWQDLKDLFRRIVGSIEYVQLFFDESGKARGCGIVEFKDPENVQKALEKM 118
      V+ISNIPYD +WQ +KDL R  VG + YV+LF D  GK+RCCG+VEFKD E V+KALE M
Sbjct: 122 VFISNIPYDMKWQAIKDLMREKVGEVTYVELFKDAEGKSRGCGVVEFKDEEFVKKALETM 181

Query: 119  NRYEVNGRELVVKEDHGEQRDQYGRIVRDGGGGGGGGGGVQGGNGGNGGGGGGGGRDHMD 178
      N+Y+++GR L +KED  + + + R GG  GG      H+
Sbjct: 182 NKYDLSGRPLNIKEDPDGENARRA-LQRTGGSFPGG-----HVP 219

Query: 179  DRDRGFSSRRDDRLSGRNFNFMMSNDYNNSSNYNLYGLSASFLESGLISGPLHNKV FVAN 238
      D  G      L  NN N+  +N      +G L + +FVAN
Sbjct: 220 DMGSGLMNLPPSIL---NNPNIPPEVISNLQ-----AGRLGSTIFVAN 259

Query: 239  LDYKVDNKKLQVFKLAGKVQSVDSL DKEGNSRGFAVIEYDHPVEAVQAISM LDRQMLF 298
      LD+KV  KKLK+VF +AG V+  D+  DK+G SRG  + ++  +EAVQAISM + Q LF
Sbjct: 260 LDFKVGWKKLKEVFSIAGTVKRADIKEDKD GKS RGMGTVTTFEQAI EAVQAISM FNQQLF 319

Query: 299  DRRMTVRLD--RIPDK-----NEGIKLPEGLGGVGIGLGPNGEPLRDVAHNL PNGGQSQ 350
      DR M V++D  +P +      + +LP GLGG+G+GLGP G+P+  N+
Sbjct: 320 DRPMHV KMDKSV PHEEYRSHDGKTPQLPRGLGGIGMGLPGGPQPISASQLNI----- 372

Query: 351  GQLLGNAQQGSQ LGSVGSQPNSSAVSNATTNLLNNLTGVMFGNHAAVQSPVAPVQKPSL 410
      G ++GN  G      + G  FG      +
Sbjct: 373 GGVMGNLGP GGM-----GMDGPGFGG-----MNRI 397

Query: 411  GNNTGSGGLNLNNLNPSILA AVVGNLGNQG--GNLSNPLLSSSL-----SNLGLNLGNS 462
      G  G GGL  N      +G G G G L  ++SS+      ++G+N G
Sbjct: 398 GGGIGFGGLEAMN-----SMGGFGGVGRMGELYRGAMTSSMERDFGRGDIGINRGFG 449

Query: 463  GNDDNLPPSNVGLSNNYSSGGTGGGNSYSSGNNSGGGGSSN-----LGYNAYSSS-G 514
      +  L + +G      +G G N  G+  SGG GS N      +G +  SSS
Sbjct: 450 DSFGRLGSAMIG----GFAGRIGSSNMGPVGSGISGGMGSMNSVTGGMGMGLDRMSSSFD 505

Query: 515  GMGGGNGGVGV DGN DYNTGNPLDVYGGGNSVGNNSVGSANAVGASRKSDTIIKNVPITC 574
      MG G G +  D + G      G G      +GS      K + I ++N+P
Sbjct: 506 RMGP GIGAILERSIDMDRGFLSGPMGSGM---RERIGS-----KGNQIFVRNLPFDL 554

Query: 575  TWQTLRDKFREIGDVKFAEI-----RGNDVGVVRFFKERDAELALMDGSRLDGRNIKV 629
      TWQ L++KF + G V FAEI      +  G VRF      AE A  +M+G ++ GR I V
Sbjct: 555 TWQKLKEKFSQC GHVMFAEIKMENGKSKGCGTVRFDSPEAEKACRIMNGIKISGREIDV 614

```

Score = 68.6 bits (166), Expect = 2e-10
Identities = 41/114 (35%), Positives = 67/114 (57%), Gaps = 6/114 (5%)

Query: 20 GRGARGSRFTDADGNGNGAGSQGGGVAARDRSRERRNCRVYISNIPYDYRWQDLKDLFRR 79
G GA R D D G +G G G+ R+R + N ++++ N+P+D WQ LK+ F +
Sbjct: 510 GIGAILERSIDMD-RGFLSGPMGSGM--RERIGSKGN-QIFVRNLPFDLTWQKLKEKFSQ 565

Query: 80 IVGSIEYVQLFFDESGKARGCGIVEFKDPENVQKALEKMNRYEVNGRELVVKED 133
G + + ++ E+GK++GCG V F PE+ +KA MN +++GRE+ V+ D
Sbjct: 566 C-GHVMFAEIKM-ENGKSKGCGTVRFDSPESAEEKACRIMNGIKISGREIDVRLD 617

Score = 56.2 bits (134), Expect = 1e-06
Identities = 46/180 (25%), Positives = 76/180 (41%), Gaps = 21/180 (11%)

Query: 139 DQYGRIVRDGGGGGGG-----GGGVQGGNGGNNGGGGGGRDHMDRDRGRFSRRD 188
D +GR+ GG G G G+ GG G N GG G +D F R
Sbjct: 450 DSFGRLGSAMIGGFAGRIGSSNMGPVSGISGGMGSMNSVTGGMGMG-LDRMSSSFDRM- 507

Query: 189 DDRLSGRNNFNMMNSNDYNNSSNYNLYGLSASFLESIGSPLHNKV FVANLDYKVDNKKL 248
G ++ + + + + E +G G N++FV NL + + +KL
Sbjct: 508 -----GPGIGAILERSIDMDRGFLSGPMGSGMRERIGSKG---NQIFVRNLPFDLTWQKL 559

Query: 249 KQVFKLAGKVQSVDSL DKEGNSRGFAVIEYDHPVEAVQAISMLDRQMLFDRRMTVRLDR 308
K+ F G V ++ ++ G S+G + +D P A +A +++ + R + VRLDR
Sbjct: 560 KEKFSQCGHVMFAEIKMEN-GKSKGCGTVRFDSPESAEEKACRIMNGIKISGREIDVRLDR 618

Homology to human protein BAB14421.1 (GenBank Accession Number)

>dbj|BAB14421.1| (AK023133) unnamed protein product [Homo sapiens],
Length = 576

Score = 242 bits (618), Expect = 1e-62
Identities = 206/654 (31%), Positives = 289/654 (43%), Gaps = 160/654 (24%)

Query: 1 MSMDASNSVESREKERDRRGAR-GSRFTDADGNGN-GAGSQGGGVAARDRSRERRNCR 58
+ M+ S + + + + G++ +RF + N G G + G RN R
Sbjct: 52 VKMENDESAKEEKSDLKEKSTGSKKANRFHPYSKDKNSGTGEKKG-----PNRN-R 101

Query: 59 VYISNIPYDYRWQDLKDLFRRIVGSIEYVQLFFDESGKARGCGIVEFKDPENVQKALEKM 118
V+ISNIPYD +WQ +KDL R VG + YV+LF D GK+RGCG+VEFKD E V+KALE M
Sbjct: 102 VFISNIPYDMKWQAIDLMREKVGEVTVYELFKDAEGKSRGCGVVEFKDEEFVKKALETM 161

Query: 119 NRYEVNGRELVVKED-HGEQRDQYGRIVRDGGGGGGGGGGVQGGNGGNNGGGGGGGGRDHM 177
N+Y+++GR L +KED GE + + R GG GG H+
Sbjct: 162 NKYDLSGRPLNIKEDPDGENARRASQ--RTGGSFPGG-----HV 198

Query: 178 DDRDRGFSRRDDRLSGRNNFNMMNSNDYNNSSNYNLYGLSASFLESIGSPLHNKV FVA 237
D G L NN N+ +N +G L + +FVA
Sbjct: 199 PDMGSGLMNLPPSIL---NNPNIPPEVISNLQ-----AGRLGSTIFVA 238

Query: 238 NLDYKVDNKKLKQVFKLAGKVQSVDSL DKEGNSRGFAVIEYDHPVEAVQAISMLDRQML 297
NLD+KV KKLK+VF +AG V+ D+ DK+G SRG + ++ +EAVQAISM + Q L
Sbjct: 239 NLDKFGVWKKLKEVFSTAGTVKRA DIKEDKDGKSRGMGTVTFEQAIEAVQAISMFGQFL 298

Query: 298 FDRRMTVRLD--RIPDK-----NEG IKLPEGLGGVGIGLGPNGEPLRDVAHNLPNGGQS 349

FDR M V++D +P + + +LP GLGG+G+GLGP G+P+ N+
 Sbjct: 299 FDRPMHVKMDDKSVPH EYRSHDGTKPQLPRGLGGIGMGLGPGGQPISASQLNI----- 352
 Query: 350 QGQLLGNAQQGSQ LGSVGSQPNSSAVSNATTNLLNNLTGVMFGNHAAVQSPVPVAPVQKPS 409
 G ++GN G + G FG
 Sbjct: 353 -GGVMGNLGP GGM-----GMDGPGFGG-----MNR 376
 Query: 410 LGNNTGSGGLN LNNLNP SILAAVVG NLGNQG--GNLSNPLLSSSL-----SNLGLNLGN 461
 +G G GGL N +G G G G L ++SS+ ++G+N G
 Sbjct: 377 IGGGIGFGGLEAMN-----SMGGFGGVGRMGEL YRGAMTSSMERDFGRGDIGINRG- 427
 Query: 462 SGNDNLPPSNVGLSN NYSSGGTGGGNSYSSGNNYSGGGSSNLGYNAYSSS-GGMGGGN 520
 G S GG GG NS + G +G + SSS MG G
 Sbjct: 428 -----FGDSFGRLGGGMGGMNSVT-----GGMGMGLDRMSSSFDRMGPGI 467
 Query: 521 GGVGVDGNDYNTGNPLDVYGGG SNVGN SNVGSANAVGASRKSDTII IKNVPITCTWQTLR 580
 G + D + G G G +GS K + I ++N+P TWQ L+
 Sbjct: 468 GAILERSIDMDRGFLSGPMGSGM---RERIGS-----KGNQIFVRNL PFDLTWQKLK 516
 Query: 581 DKFREIGDVKFAEI-----RGNDVGVRFFKERDAELAIALMDGSRLDGRNIKV 629
 +KF + G V FAEI + G VRF AE A +M+G ++ GR I V
 Sbjct: 517 EKFSQCGHVMFAEIKMENGKSKGCGTVRFDSPESA EKACRIMNGIKISGREIDV 570

Score = 72.8 bits (177), Expect = 1e-11
 Identities = 82/348 (23%), Positives = 133/348 (37%), Gaps = 96/348 (27%)

Query: 54 RRNCRVYISNIPYD YRWQDLKDLFR RIVGSIEYVQLFFDESGKARGCGIVEFKDPENVQK 113
 R ++++N+ + W+ LK++F I G+++ + D+ GK+RG G V F+ +
 Sbjct: 230 RLGSTIFVANLDFKVGWKKLKEVFS-IAGTVKRADIKEDKD GKS RGMGTVTTFEQ AIEAVQ 288
 Query: 114 ALEKMNR YE VNGREL VVKED-----HGEQRDQYGRIVRDGGGGGGGG----- 155
 A+ N + R + VK D H E R G+ + G GG G
 Sbjct: 289 AISMFNGQFLFDRPMHVKMDDKSVPH EYRSHDGTKPQLPRGLGGIGMGLGPGGQPISAS 348
 Query: 156 ----GGVQG-----GNGGNNGGGG-----GGRDHMDDRDRGF 184
 GGV G G GG N GGG GG M + RG
 Sbjct: 349 QLNIGGVMGNLGP GGMGMDGPGFGGMNRIGGGIGFGGLEAMNSMGGFGGVGRMGEL YRGA 408
 Query: 185 SRRDDRLSGRNFMMS-----NDYNNSSNYNLYGLSASFLES LG--- 225
 +R GR + + N L +S+SF + +G
 Sbjct: 409 MTSSMERDFGRGDIGINRGFGDSFGRLGGGMGGMNSVTGGMGMGLDRMSSSF-DRMGPGI 467
 Query: 226 -----ISGPLH-----NKVFVANLDYKVDNKKLKQVFKLAGKVQS 260
 +SGP+ N++FV NL + + +KLK+ F G V
 Sbjct: 468 GAILERSIDMDRGFLSGPMGSGMRERIGSKGNQIFVRNL PFDLTWQKLKEKFSQCGHVMF 527
 Query: 261 VDLSLDKEGNSRGFAVIEYDHPVEAVQAISMLDRQMLFDRRMTVRLDR 308
 ++ ++ G S+G + +D P A +A +++ + R + VRLDR
 Sbjct: 528 AEIKMEN-GKSKGCGTVRFDSPESA EKACRIMNGIKISGREIDVRLDR 574

Score = 68.6 bits (166), Expect = 2e-10
 Identities = 41/114 (35%), Positives = 67/114 (57%), Gaps = 6/114 (5%)

Query: 20 GRGARGSRFTDADGNGNGAGSQGGGVAARDRSRERRNCRVYISNIPYD YRWQDLKDLFR 79
 G GA R D D G +G G G+ R+R + N +++ N+P+D WQ LK+ F +
 Sbjct: 466 GIGAILERSIDMD-RGFLSGPMGSGM---RERIGSKGN-QIFVRNL PFDLTWQKLKEKFSQ 521
 Query: 80 IVGSIEYVQLFFDESGKARGCGIVEFKDPENVQKALEKMNR YE VNGREL VVKED 133

G + + ++ E+GK++GCG V F PE+ +KA MN +++GRE+ V+ D
 Sbjct: 522 C-GHVMFAEIKM-ENGKSKGCGTVRFDSPEAEKACRIMNGIKISGREIDVRLD 573

Homology to human protein NP057216.1 (GenBank Accession Number)

ref|NP_057216.1| (NM_016132) myelin gene expression factor 2 [Homo sapiens]
 gb|AAD43038.1| (AF106685) myelin gene expression factor 2 [Homo sapiens]
 Length = 547

Score = 238 bits (607), Expect = 2e-61
 Identities = 204/659 (30%), Positives = 295/659 (43%), Gaps = 150/659 (22%)

Query: 3 MDASNSVESREKERDRRGRGAR-GSRFTDADGNGN-GAGSQGGGVAARDRSRERRNCRVY 60
 M+ S + + + + G++ +RF + N G G + G RN RV+
 Sbjct: 1 MENDESAKEEKSDLKEKSTGSKKANRFHPYSKDKNSGTGEKKG-----PNRN-RVF 50

Query: 61 ISNIPYDYRWQDLKDLFRRIVGSIEYVQLFFDESGKARGCGIVEFKDPENVQKALEKMNR 120
 ISNIPYD +WQ +KDL R VG + YV+LF D GK+RCCG+VEFKD E V+KALE MN+
 Sbjct: 51 ISNIPYDMKWQAIKDLMREKVGEVTYVELFKDAEGKSRCCGVVEFKDEEFVKKALETMNK 110

Query: 121 YEVNGRELTVKEDHGEQORDQYGRIVRDGGGGGGGGGGVQGGNGGNGGGGGGGGRDHMDDR 180
 Y+++GR + +KED + + + R G QG + + G G
 Sbjct: 111 YDLSGRRVNIKEDPDGENARRA-LQRTGTS-----FQGS HASDVGSG----- 151

Query: 181 DRGFSRRDDRLSGRRNFMMSNDYNNSSNYNLYGLSASFLESGLISGPLHNKVFVANLD 240
 N+ + NN + + +L +G L + +FVANLD
 Sbjct: 152 -----LVNLPSPILNNPN-----IPPEVISNLQ-AGRLGSTIFVANLD 188

Query: 241 YKVDNKKLKQVFKLAGKVQSVDSLSDKEGNSRGFAVIEYDHPVEAVQAISM LDRQMLFDR 300
 +KV KKLK+VF +AG V++ DK+G SRG + ++ +EAVQAISM + Q LFDR
 Sbjct: 189 FKVGWKKLKEVFSIAGTVKAGSYKEDKD GKS RGMGTVTTFEQAI EAVQAISM FNQQLFDR 248

Query: 301 RMTVRLD-----RIPDKNEGILKPEGLGGVGIGLGPNGEPLRDVAHNL PGGQSQG 351
 M V++D R PD + +LP GLGG+G+GLGP G+P+ N+ G
 Sbjct: 249 PMHVKMDDKSPHEEYRSPD-GKTPQLPRGLGGIGMGLGPGGQPISASQLNI-----G 300

Query: 352 QLLGNAQQGSQ LGSVGSQPNSSAVSNATTNLLNNLTGVMFGNHA AVQSPVAPVQKPSLG 411
 ++GN G + G FG +G
 Sbjct: 301 GVMGNLGP GGM-----GMDGPGFGG-----MNRIG 325

Query: 412 NNTGSGGLN LNNLNP SILA AVVGNLGNQG--GNLSNPL LSSSL-----NLGLNLGNSG 463
 G GGL N +G G G G L ++SS+ ++GL+ G
 Sbjct: 326 GGIGFGGLEAMN-----SMGGFGGVGRMGELYRGAMTSSMERDFGHRDIGLSRGFGD 377

Query: 464 NDDNLPPSNVGLSN NYSSGGTGGGNSYSSGNNYSGGGGSSN-----LGYNAYSSS-GG 515
 + L + +G +G G N G+ SGG GS N +G + SSS
 Sbjct: 378 SFGR LGSAMIG----GITGRIGSSNMGPVSGSGISGGMGSMNSVTGGMGMLDRMSSSFDR 433

Query: 516 MGGGNGGVGVGDNDYNTGNPLDVYGGGNSVGNVGSANAVGASRKS DTII IKNPITCT 575
 MG G G + D + G G G +GS K + I ++N+P T
 Sbjct: 434 MGPGIGAILERSIDMDRGFLSGPMGSGM---RERIGS-----KGNQIFVRNL PFDLT 482

Query: 576 WQTLRDKPREIGDVKFAEI-----RGNDVGVVRFFKERDAELALALMDGSRLDGRNIKV 629
 WQ L++KF + G V FAEI + G VRF AE A +M+G ++ GR I V
 Sbjct: 483 WQKLKEKFSQCGHVMFAEIKMENGKSKGCGTVRFDSPEAEKACRIMNGIKISGREIDV 541

Score = 68.6 bits (166), Expect = 2e-10
Identities = 41/114 (35%), Positives = 67/114 (57%), Gaps = 6/114 (5%)

Query: 20 GRGAGSRFTDADGNGNGAGSQGGGVAARDRSRERRNCRVYISNIPYDYRWQDLKDLFRR 79
G GA R D D G +G G G+ R+R + N +++ N+P+D WQ LK+ F +
Sbjct: 437 GIGAILERSIDMD-RGFLSGPMGSGM--RERIGSKGN-QIFVRNLPFDLTWQKLKEKFSQ 492

Query: 80 IVGSIEYVQLFFDESCKARGCGIVEFKDPENVQKALEKMNRYEVNGRELNVKED 133
G + + ++ E+GK++GCG V F PE+ +KA MN +++GRE+ V+ D
Sbjct: 493 C-GHVMFAEIKM-ENGKSKGCGTVRFDSPEAEKACRIMNGIKISGREIDVRLD 544

Score = 55.5 bits (132), Expect = 2e-06
Identities = 41/157 (26%), Positives = 69/157 (43%), Gaps = 11/157 (7%)

Query: 152 GGGGGGVQGGNGGNGGGGGGGGRDHMDRDRGFSRRDDRLSGRNNFNMMNSNDYNNSSNY 211
G G G+ GG G N GG G +D F R G ++ + +
Sbjct: 400 GPVGSISGGMGSMNSVTGGMGMG-LDRMSSSFDRM-----GPGIGAILERSIDMDRGF 452

Query: 212 NLYGLSASFLESGLISGPLHNKVFVANLDYKVDNKKLKQVFKLAGKVQSVDSLSDKEGNS 271
+ + E +G G N++FV NL + + +KLK+ F G V ++ ++ G S
Sbjct: 453 LSGPMGSGMRERIGSKG---NQIFVRNLPFDLTWQKLKEKFSQCGHVMFAEIKMEN-GKS 508

Query: 272 RGFVIEYDHPVEAVQAISMLDRQMLFDRRMTVRLDR 308
+G + +D P A +A +++ + R + VRLDR
Sbjct: 509 KGCCTVRFDSPESAEEKACRIMNGIKISGREIDVRLDR 545

Figure 15B. Multiple Sequence Alignment (ClustalW 1.83)

```

CG9373 Dm -----
KIAA1341 Hs PLSRSEPLSSGGRGGGSGGGMADANKAEVPGATGGDSPHLQPAEPPGEPRREPHPAEAEK
MyEF-2 Hs -----
FLJ13071 Hs -----MADANKAEVPGATGGDSPHLQPAEPPGEPRREPHPAEAEK

CG9373 Dm ---MSMDASNSVESREKERDRRGARGSRFTDADGNGNGAGSQGGGVAARDRSRERRNC
KIAA1341 Hs QQPQHSSSSNGVKMENDESAAKEEKSDLKEKSTGSKKANRFHPYSKDKNSGTGEKKGPNRN
MyEF-2 Hs -----MENDESAAKEEKSDLKEKSTGSKKANRFHPYSKDKNSGTGEKKGPNRN
FLJ13071 Hs QQPQHSSSSNGVKMENDESAAKEEKSDLKEKSTGSKKANRFHPYSKDKNSGTGEKKGPNRN

CG9373 Dm RVYISNIPYDYRWQDLKDLFRRIVGSIEYVQLFFDESCKARGCGIVEFKDPENVQKALEK
KIAA1341 Hs RVFISNIPYDMKWQAIKDLMREKVGVEVTVYELFKDAEGKSRGCGVVEFKDEEFVKALET
MyEF-2 Hs RVFISNIPYDMKWQAIKDLMREKVGVEVTVYELFKDAEGKSRGCGVVEFKDEEFVKALET
FLJ13071 Hs RVFISNIPYDMKWQAIKDLMREKVGVEVTVYELFKDAEGKSRGCGVVEFKDEEFVKALET

CG9373 Dm MNRYEVNGRELNVKEDHGEQRDQYGRIVRDGGGGGGGGGGGVQGGNGGNGGGGGGGGRDHM
KIAA1341 Hs MNKYDLSGRPLNIKEDPDGENARR-----ALQRTGGSFPGGHVPDMGSG-----
MyEF-2 Hs MNKYDLSGRRVNIKEDPDGENARR-----ALQRTGTSFQGSASDVGSG-----
FLJ13071 Hs MNKYDLSGRPLNIKEDPDGENARR-----ASQRTGGSFPGGHVPDMGSG-----

CG9373 Dm DDRDRGFSRRDDRLSGRNNFNMMNSNDYNNSSNYNLYGLSASFLESGLISGPLHNKVFVA
KIAA1341 Hs -----LMNLPPSILNNPNIPPEVISNLQ----AGRLGSTIFVA
MyEF-2 Hs -----LVNLPPSILNNPNIPPEVISNLQ----AGRLGSTIFVA
FLJ13071 Hs -----LMNLPPSILNNPNIPPEVISNLQ----AGRLGSTIFVA

```

CG9373 Dm NLDYKVDNKKLKQVFKLAGKVQSVDLSDKEGNSRGFAVIEYDHPVEAVQAI SMLDRQML
 KIAA1341 Hs NLDKFKVGWKKLKEVFSIAGTVKRADIKEDKD GKS SRGMGTVTTFEQAI EAVQAI SMFNGQFL
 MyEF-2 Hs NLDKFKVGWKKLKEVFSIAGTVKAGSYKEDKD GKS SRGMGTVTTFEQAI EAVQAI SMFNGQFL
 FLJ13071 Hs NLDKFKVGWKKLKEVFSIAGTVKRADIKEDKD GKS SRGMGTVTTFEQAI EAVQAI SMFNGQFL

CG9373 Dm FDRRMTVRLDRI PDKN EGIK-----LPEGLGGVGIGLGPNGEPLRDVAHNL PNGGQS
 KIAA1341 Hs FDRPMHVKMDDKSVPHEEYRSHDGKTPQLPRGLGGIGMGLGPGGQPISASQLNIG-----
 MyEF-2 Hs FDRPMHVKMDDKSVPHEEYRSPDGKTPQLPRGLGGIGMGLGPGGQPISASQLNIG-----
 FLJ13071 Hs FDRPMHVKMDDKSVPHEEYRSHDGKTPQLPRGLGGIGMGLGPGGQPISASQLNIG-----

CG9373 Dm QQQLLGNAQQGSQ LGSVGSQPNSSAVSNATTNLLNNLTG-VMFGNHA AVQPSVAPVQKP
 KIAA1341 Hs -----GVMGNLG--PGGMGMDGPGFGGMNRIGGGIGFGGLEAMN-----
 MyEF-2 Hs -----GVMGNLG--PGGMGMDGPGFGGMNRIGGGIGFGGLEAMN-----
 FLJ13071 Hs -----GVMGNLG--PGGMGMDGPGFGGMNRIGGGIGFGGLEAMN-----

CG9373 Dm SLGNNTGSGGLN LNNLNP SILAAVVGNLGNQGGNLSNPL LSSSLSNLGLNLGNSGNDNL
 KIAA1341 Hs SMGGFGGVG--RMGELYRGAMTSSMERDFGRGDIGINRGFGDSFGRLGSAM-IGGFAGRI
 MyEF-2 Hs SMGGFGGVG--RMGELYRGAMTSSMERDFGHRD IGLSRGFGDSFGRLGSAM-IGGITGRI
 FLJ13071 Hs SMGGFGGVG--RMGELYRGAMTSSMERDFGRGDIGINRGFGDSFGRLG-----

CG9373 Dm PPSNVGLSNNYSSGGTGGGNSYSSGNNYSGGGSSNLGYNAYSSSGMGGGNGGVGDGN
 KIAA1341 Hs GSSNMGPVGSGISGGMGSMNSVTGGMGMLDRMSSSFDR-----MGP GIGAILERSI
 MyEF-2 Hs GSSNMGPVGSGISGGMGSMNSVTGGMGMLDRMSSSFDR-----MGP GIGAILERSI
 FLJ13071 Hs -----GGMGGMNSVTGGMGMLDRMSSSFDR-----MGP GIGAILERSI

CG9373 Dm DYNTGNPLDVYGGGSNVGNSNVGSANAVGASRKS DTII IKNVPITCTWQTLRDKFREIGD
 KIAA1341 Hs DMDRG-----FLSGPMGSGMRERIGSKGNQIFVRNL PFDLTWQKLKEKFSQCGH
 MyEF-2 Hs DMDRG-----FLSGPMGSGMRERIGSKGNQIFVRNL PFDLTWQKLKEKFSQCGH
 FLJ13071 Hs DMDRG-----FLSGPMGSGMRERIGSKGNQIFVRNL PFDLTWQKLKEKFSQCGH

CG9373 Dm VKFAEIRGND-----VGVRFFKERDAELAIALMDGSRLDGRNIKVTYF---
 KIAA1341 Hs VMFAEIKMENGKSKGCGTVRFDSPESA EKACRIMNGIKISGREIDVRLDRNA
 MyEF-2 Hs VMFAEIKMENGKSKGCGTVRFDSPESA EKACRIMNGIKISGREIDVRLDRNA
 FLJ13071 Hs VMFAEIKMENGKSKGCGTVRFDSPESA EKACRIMNGIKISGREIDVRLDRNA

Figure 16. Expression of CG9373 Homologs in Mammalian Tissues

Figure 16A. Real-time PCR analysis of myelin gene expression factor 2 (MEF-2) expression in wild type mouse tissues (DCt Pancreas = 20,90)

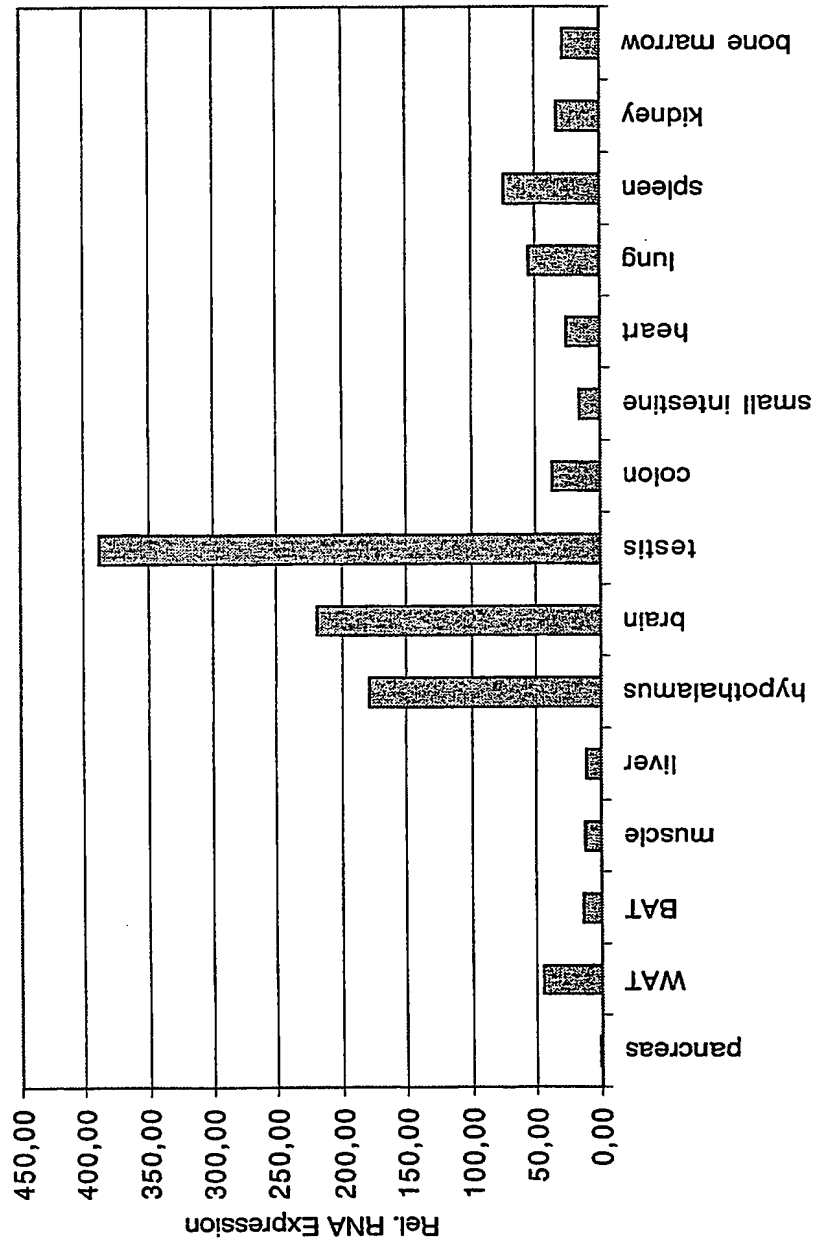


Figure 16B. Real-time PCR analysis of myelin gene expression factor 2 (MEF-2) expression in different mouse models

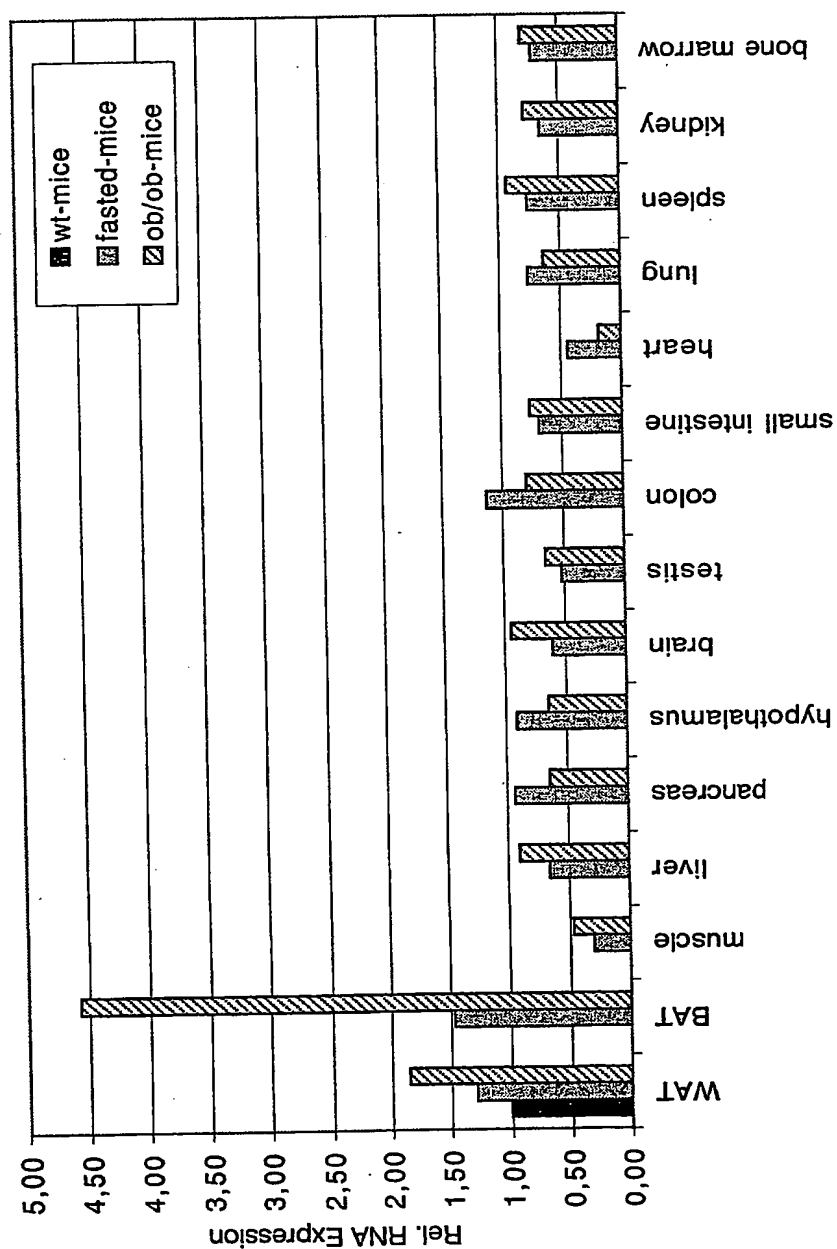


Figure 16C. Real-time PCR analysis of myelin gene expression factor 2 (MEF-2) expression in mice fed with a high fat diet compared to mice fed with a standard diet

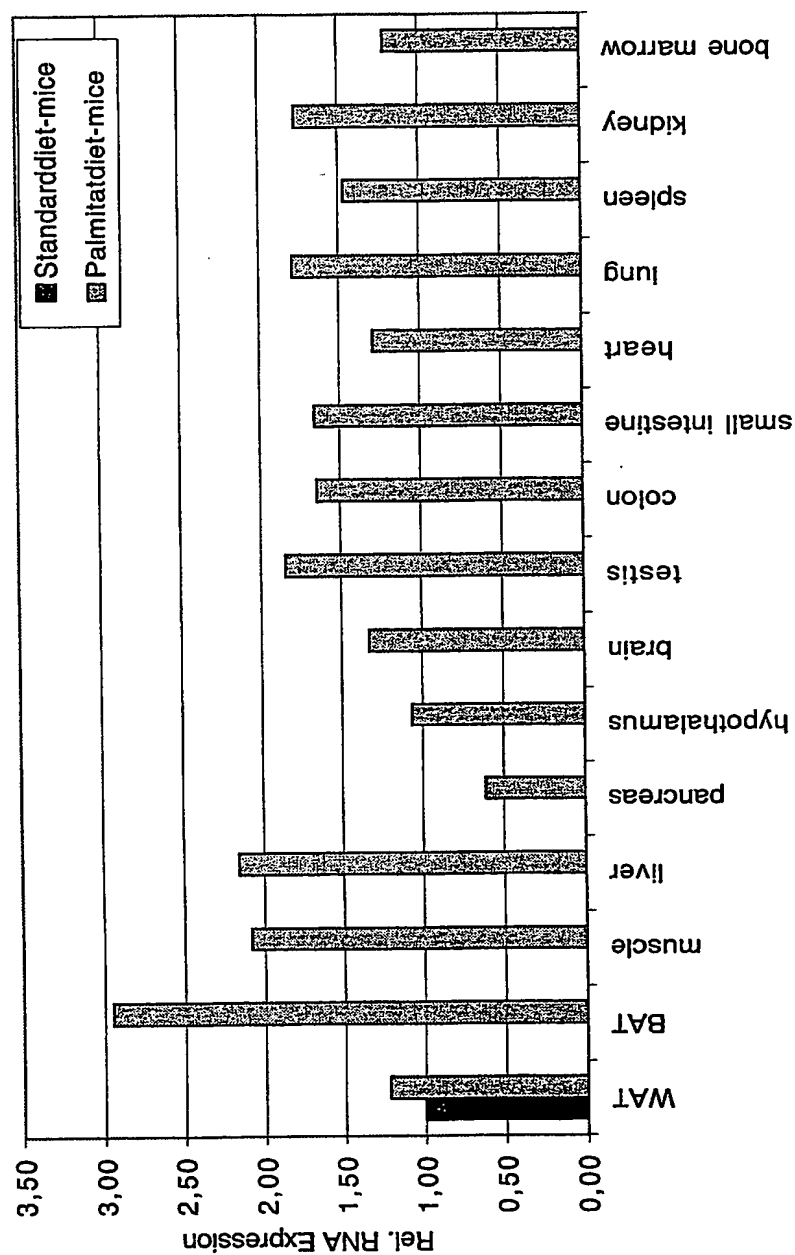


Figure 17. Triglyceride content of a *Drosophila cpo* (GadFly Accession Number CG18434) mutant

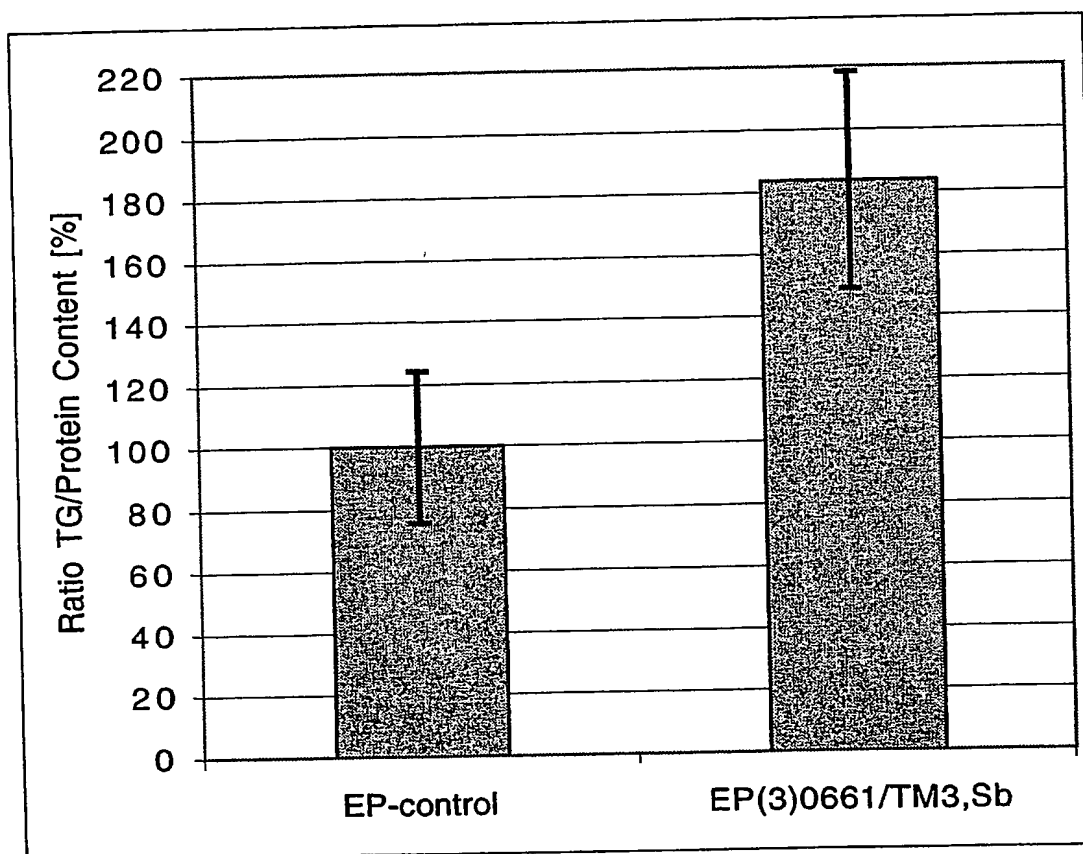


Figure 18. Molecular organisation of the *cpo* gene (GadFly Accession Number CG18434)

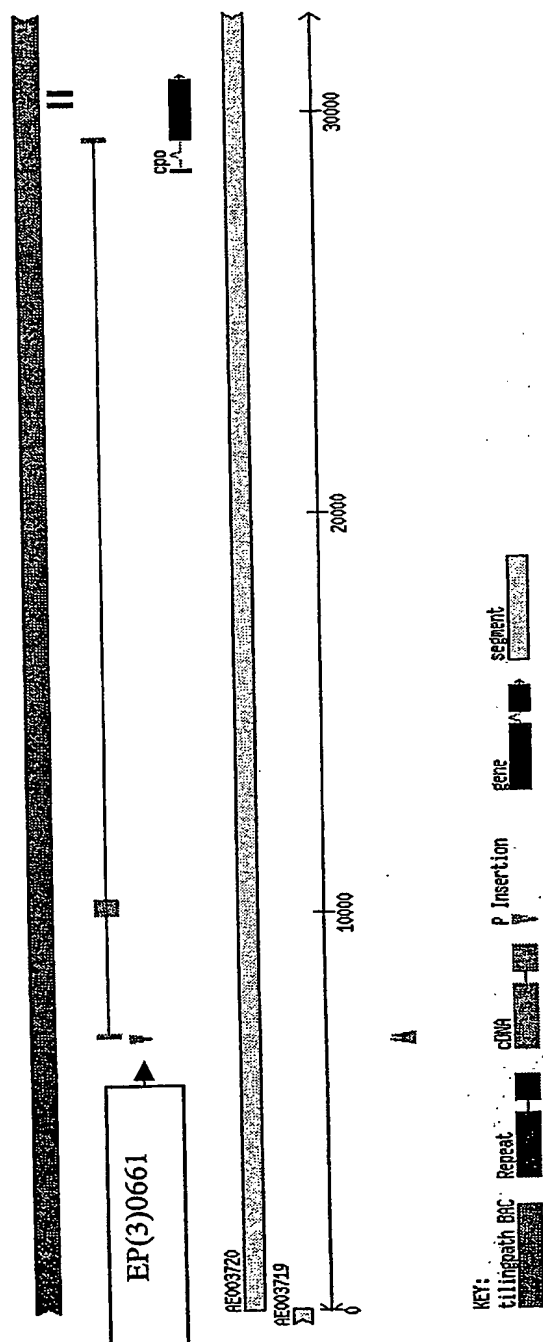


Figure 19. Homology of *Drosophila cpo* (GadFly Accession Number CG31243 and CG18434) to human RNA binding proteins with multiple splicing

Figure 19A. Multiple Sequence Alignment (ClustalW 1.83)

```

cpo Dm      LVKIAN YQDLLGSHHQLLIAATAAAAAAAAAAEPQLQLQHLLPAAPTTPAVISNPINSIGP
NP_006858 Hs -----
IPI00161102 Hs -----

cpo Dm      INQISSSSHPSNNNQAVFEKAITISSIAIKRRPTLPQTPASAPQVLSPPSKRQCAAAVS
NP_006858 Hs -----
IPI00161102 Hs -----

cpo Dm      VLPVTVFPVPVPVSVPLPVSVFPVPVSVKGHPISHTHQIAHTHQISHSHPI SHPHHHQLSFA
NP_006858 Hs -----
IPI00161102 Hs -----

cpo Dm      HPTQFAAAVA AHHQQQQQQAQQQQQAVQQQQQQAVQQQQVAYAVAASPOLQQQQQQQQH
NP_006858 Hs -----
IPI00161102 Hs -----

cpo Dm      RLAQFNQAAAAALLNQHLQQQHQAQQQQHQAQQQSLAHYGGYQLHRYAPQQQQQHILLSS
NP_006858 Hs -----
IPI00161102 Hs -----

cpo Dm      GSSSSKHNSNNNSNTSAGAASAAVPIATSVA AVPTTGGSLPDSPA HESHSHESNSATASA
NP_006858 Hs -----
IPI00161102 Hs -----

cpo Dm      PTTSPAGSVTSAAPTATATAAAAGSAAATAAATGTPATSAVSDSNNNNLNSSSSSNSNSN
NP_006858 Hs -----
IPI00161102 Hs -----MNNNGGK

cpo Dm      AIMENQMALAPLGLSQSMDSVNTASNEEEVRTL FVSGLPMDAKPRELYLLFRAYEGYEGS
NP_006858 Hs AEKENTPSEANL-----QEEEVRTL FVSGLPLDIKPRELYLLFRPFKGYEGS
IPI00161102 Hs -----QVRTLFVSGLPVDIKPRELYLLFRPFK-----

cpo Dm      LLKVT SKNGKTASPVGFVTFHTRAGAEAAKQDLQGV RFDPMPTIRLEFAKSNTKVSKP
NP_006858 Hs LIKLT SKQ-----PVGFVSFDSRSEAEAAKNALNGIRFDPEIPQTLRLEFAKANTKMAKN
IPI00161102 Hs -----PVGFVIFDSRAGAEAAKNALNGIRFDPENPQTLRLEFAKANTKMAKS

cpo Dm      KPQPN TATTASHPALMHPLTG-----HLGGPFFPGGP ELWHHPLAYSAAAAAELPG-----
NP_006858 Hs KLVGTPNPSTPLPNTVPQFIAREPYELTVPALY PSSPEVWAPYPLYP AELAPALPPPAFT
IPI00161102 Hs KL MATPNPSNVHPALGAHFIARDPYDLMGAALIPASPEAWAPYPLYTT ELTPAISHAAFT

cpo Dm      -----AAALQHATLVHPALHPQVP---VRSYL
NP_006858 Hs YP-----ASLHAQMRWLPPSEATSQGWKSRQFC
IPI00161102 Hs YPTATAAAALHAQVRWYPSSDTTQGWKYRQFC

```

FIGURE 19B. Amino acid sequence encoded by Drosophila gene CG31243 (GadFly Accession Number), SEQ ID NO:1

>CG31243-PA (AE003720) [gene_syn=CG31243] [prot_desc=CG31243 gene product from transcript CG31243-RA]

```
1  LVKIANVQDL  LGSHHQLLIA  ATAAAAAAAA  AEPQLQLQHL  LPAAPTTPAV  ISNPINSIGP
61  INQISSSSHP  SNNNQAVFE  KAITISSIAI  KRRPTLPQTP  ASAPQVLSPS  PKRQCAAASV
121 VLPVTVVPV  PVSVPVPVS  PVPVSVKGHP  ISHTHQIAHT  HQISHSHPI  S  HPHHHQLSFA
181 HPTQFAAAVA  AHHQHQHQHQ  AQQQQQAVQQ  QQQQAVQQQQ  VAYAVAASPQ  LQQQQQQQQH
241 RLAQFNQAAA  AALLNQHLQQ  QHQHQHQHQ  AQQQSLAHYG  GYQLHRYAPQ  QQQQHILLSS
301 GSSSSKHNSN  NNSNTSAGAA  SAAVPIATSV  AAVPTTGGSL  PDSPAHESES  HESNSATASA
361 PTPSPAGSV  TSAAPTATAT  AAAAGSAAAT  AAATGTPATS  AVSDSNNNLN  SSSSSNSNSN
421 AIMENQMALA  PLGLSQSMDS  VNTASNEEEV  RTLFVSGLEP  DAKPRELYLL  FRAYEGYEGS
481 LLKVTSKNGK  TASPVGFTF  HTRAGAEAAK  QDLQGVRFDP  DMPQTIRLEF  AKSNTKVSKP
541 KPQPNTATTA  SHPALMHPLT  GHLGGPFFPG  GPWLWHHPLA  YSAAAAAELP  GAAALQHATL
601 VHPALHPQVP  VRSYL
```

Figure 20. Expression of a human *cpo* homolog in mammalian (human) tissue

Quantitative analysis of RNA binding protein with multiple splicing (RBPMS) expression in human abdominal adipocyte cells during the differentiation from preadipocytes to mature adipocytes

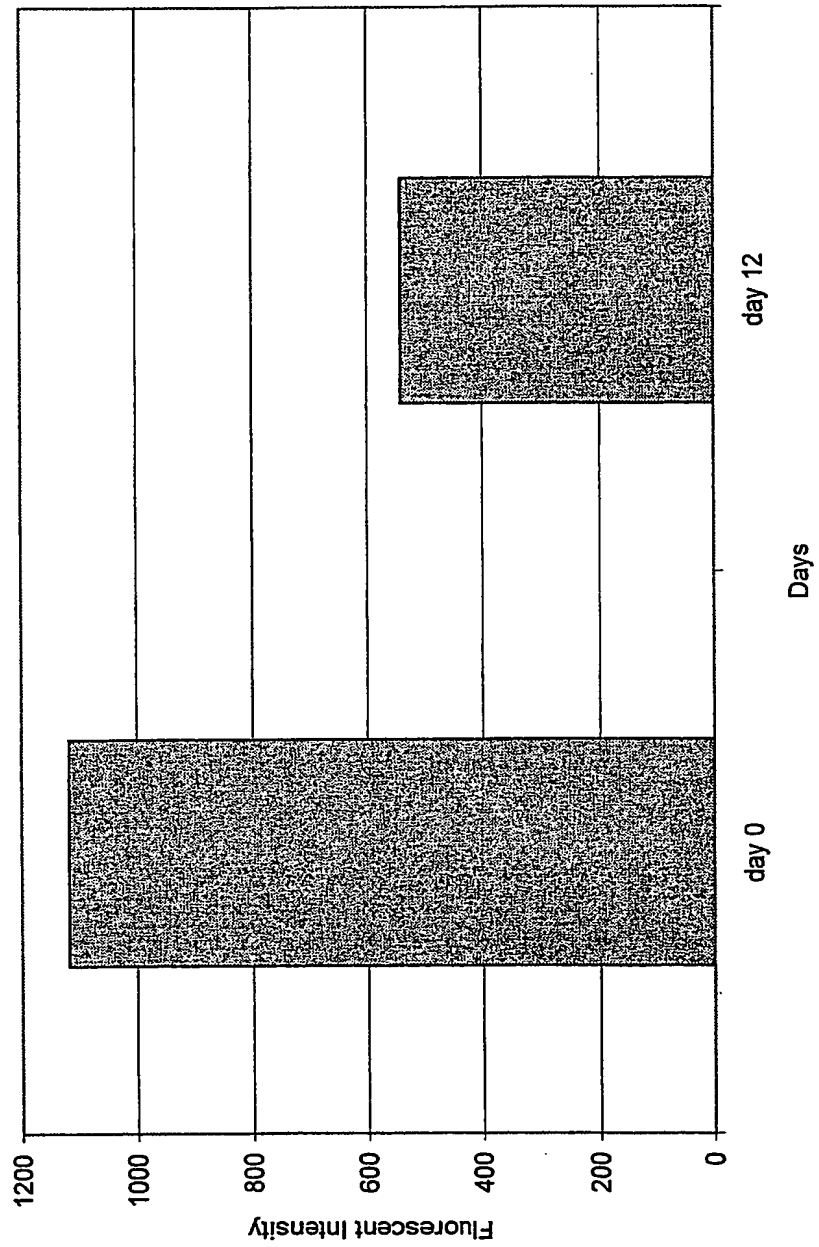


Figure 21. Triglyceride content of a *Drosophila Jafrac1* (GadFly Accession Number CG1633) mutant

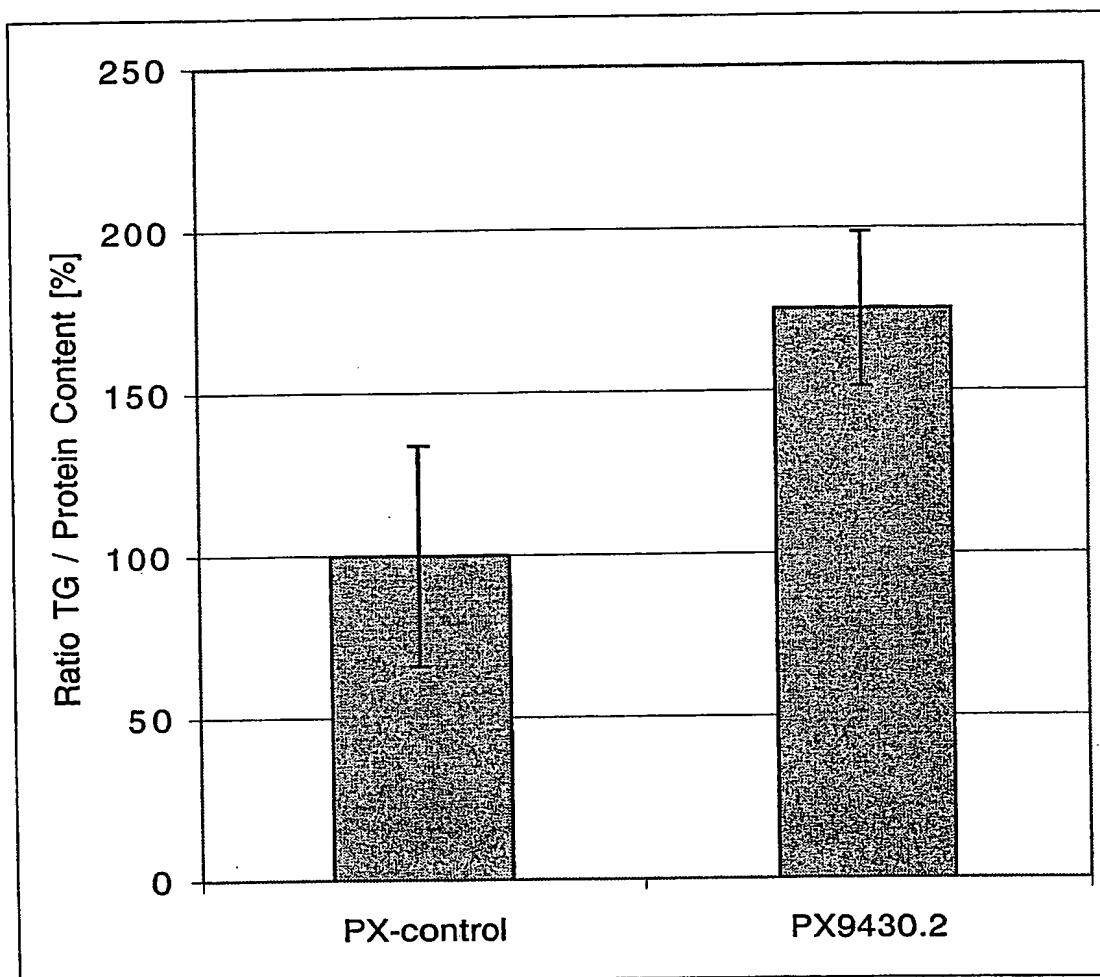


Figure 22. Molecular organisation of the *Jafracl* gene (GadFly Accession Number CG1633)

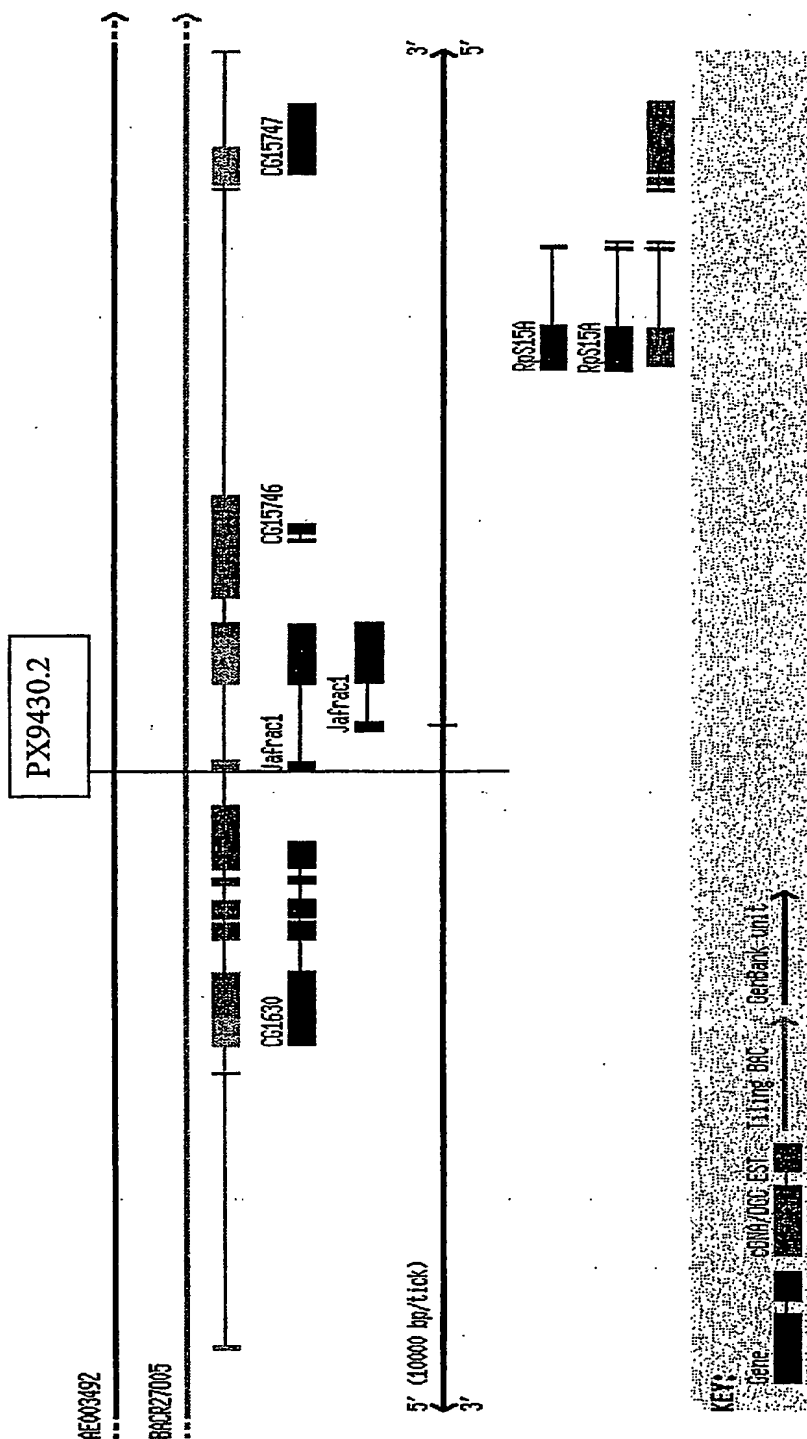


Figure 23. Homology of *Drosophila Jafrac1* (GadFly Accession Number CG1633) to human peroxiredoxin 1 and human peroxiredoxin 2 (similar to peroxiredoxin 1)

Figure 23A. BLASTP results for *Jafrac1*

Homology to human protein XP_009063.2 (GenBank Accession Number)

ref|XP_009063.2| (XM_009063) peroxiredoxin 2 [Homo sapiens]
Length = 198

Score = 283 bits (723), Expect = 9e-76
Identities = 134/188 (71%), Positives = 157/188 (83%)

```
Query: 3   QLQKPAPAFAGTAVVNGVFKDIKLSDYKGKYLVLFFYPLDFTFVCPTEIIAFSESAAEFR 62
          ++ KPAP F TAVV+G FK++KLSDYKGKY+VLFFYPLDFTFVCPTEIIAFS A +FR
Sbjct: 7   RIGKPAPDFKATAVVDGAFKEVKLSDYKGKYVVLFFYPLDFTFVCPTEIIAFSNRAEDFR 66

Query: 63  KINCEVIGCSTDSQFTHLAWINTPRKQGGLGSMIDIPLLADKSMKVARDYGVLDDEETGIPF 122
          K+ CEV+G S DSQFTHLAWINTPRK+GGLG ++IPLLAD + +++ DYGV L + GI +
Sbjct: 67  KLGCEVLGVSVDSQFTHLAWINTPRKEGGLGPLNIPLLADVTRRLSEYGV LKTDEGIAY 126

Query: 123 RGLFIIDDKQNL RQITVNDLPVGRSVEETLRLVQAFQYTDKYGEVCPANWKPQKTMVAD 182
          RGLFIID K LRQITVNDLPVGRSV+E LRLVQAFQYTD++GEVCPA WKPG T+ +
Sbjct: 127 RGLFIIDGKGVLRQITVNDLPVGRSVDEALRLVQAFQYTD EHGVECPAGWKPGSDTIKPN 186

Query: 183 PTKSKEYF 190
          SKEYF
Sbjct: 187 VDDSKEYF 194
```

Homology to human protein NP_002565.1 (GenBank Accession Number)

ref|NP_002565.1| (NM_002574) peroxiredoxin 1; Proliferation-associated gene A;
proliferation-associated gene A (natural killer-enhancing factor A) [Homo sapiens]
ref|XP_001393.2| (XM_001393) peroxiredoxin 1 [Homo sapiens]
Length = 199

Score = 281 bits (718), Expect = 3e-75
Identities = 135/185 (72%), Positives = 154/185 (82%), Gaps = 1/185 (0%)

```
Query: 7   PAPAFAGTAVV-NGVFKDIKLSDYKGKYLVLFFYPLDFTFVCPTEIIAFSESAAEFRKIN 65
          PAP F TAV+ +G FKDI LSDYKGKY+V FFYPLDFTFVCPTEIIAFS+ A EF+K+N
Sbjct: 11  PAPNFKATAVMPDGQFKDISLSDYKGKYVVFYPLDFTFVCPTEIIAFSDRAEEFKLN 70

Query: 66  CEVIGCSTDSQFTHLAWINTPRKQGGLGSMIDIPLLADKSMKVARDYGVLDDEETGIPFRGL 125
          C+VIG S DS F HLA W+NTP+KQGGLG M+IPL++D +A+DYGV L + GI FRGL
Sbjct: 71  CQVIGASVDSHFCHLAWVNTPKKQGGLGPMNIPLVSDPKRTIAQDYGV LKADEGISFRGL 130

Query: 126 FIIDDKQNL RQITVNDLPVGRSVEETLRLVQAFQYTDKYGEVCPANWKPQKTMVADPTK 185
          FIIDDK LRQITVNDLPVGRSV+ETLRLVQAFQ+TDK+GEVCPA WKPG T+ D K
Sbjct: 131 FIIDDKGILRQITVNDLPVGRSVDET LRLVQAFQFTDKHGEVCPAGWKPGSDTIKPDVQK 190

Query: 186 SKEYF 190
          SKEYF
Sbjct: 191 SKEYF 195
```

Figure 23B. Multiple Sequence Alignment (ClustalW 1.83)

Jafrac1 Dm MP-----QLQKPAPAFAGTAVV-NGVFKDIKLSDYKGKYLVLFFYPLDFTFVCPTETIIAFS
PRDX1 Hs MSSGNAKIGHPAPNFKATAVMPDGQFKDISLSDYKGKYVVFYPLDFTFVCPTETIIAFS
PRDX2 Hs MASGNARIGKPAPDFKATAVV-DGAFKEVKLSDYKGKYVVLFFYPLDFTFVCPTETIIAFS

Jafrac1 Dm ESAAEFRKINCEVIGCSTDSQFTHLAWINTPRKQGGLGSMIDPLLADKSMKVARDYGVLD
PRDX1 Hs DRAEEFKKLNCQVIGASVDSHFCHLAWVNTPKKQGGLGPMNIPLVSDPKRTIAQDYGVLK
PRDX2 Hs NRAEDFRKLGCEVLGVSVDQSQFTHLAWINTPRKEGGLGPLNIPLLADVTRRLSEYGVLK

Jafrac1 Dm EETGIPFRGLFIIDDKQNLRQITVNDLPVGRSVEETLRLVQAFQYTDKYGEVCPANWKPG
PRDX1 Hs ADEGISFRGLFIIDDKGILRQITVNDLPVGRSVDETLRLVQAFQFTDKHGEVCPAGWKPG
PRDX2 Hs TDEGIAYRGLFIIDGKGVLRLQITVNDLPVGRSVDEALRLVQAFQYTDHGEVCPAGWKPG

Jafrac1 Dm QKTMVADPTKSKEYFETTS
PRDX1 Hs SDTIKPDVQKSKEYFSKQK
PRDX2 Hs SDTIKPNVDDSKEYFSKHN

Figure 24. Expression of a human *Jafracl* homolog in mammalian (human) tissue
Quantitative analysis of Peroxiredoxin 1 (PRDX1) expression in human abdominal adipocyte cells during the differentiation from preadipocytes to mature adipocytes

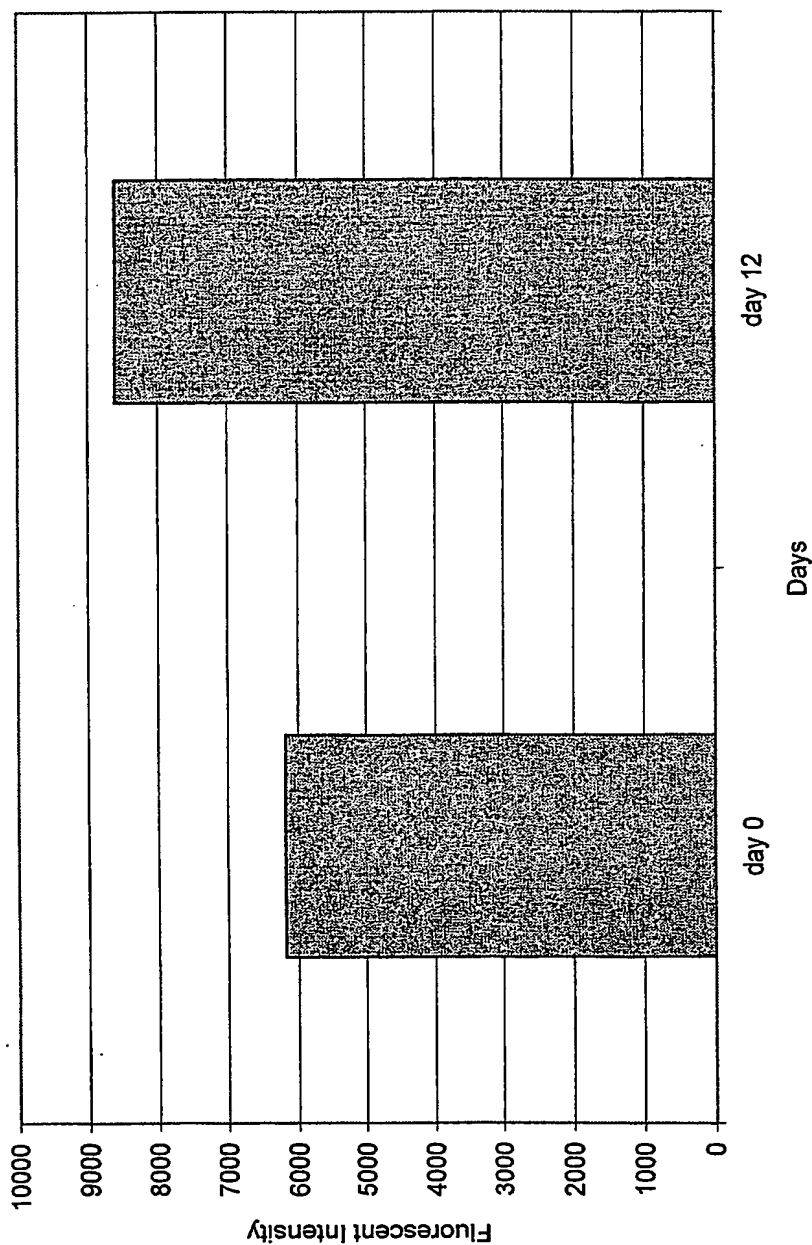


Figure 25. Triglyceride content of a *Drosophila* CG14440 (GadFly Accession Number) mutant

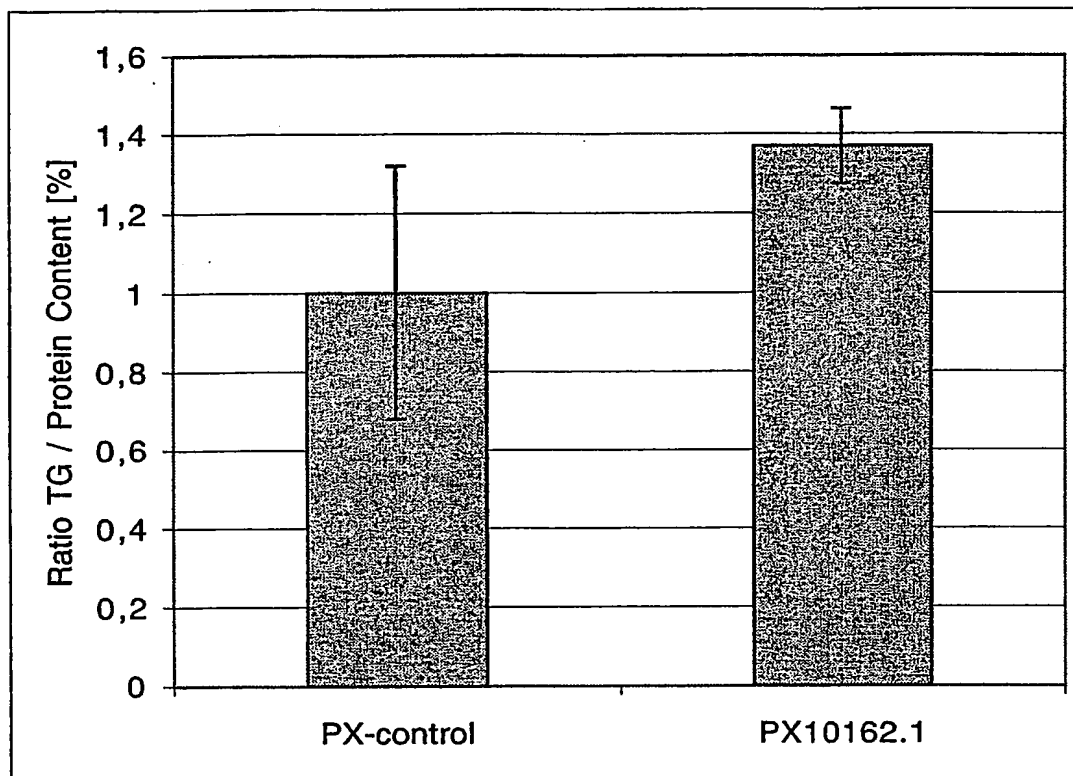


Figure 26. Molecular organization of the CG14440 gene (GadFly Accession Number)

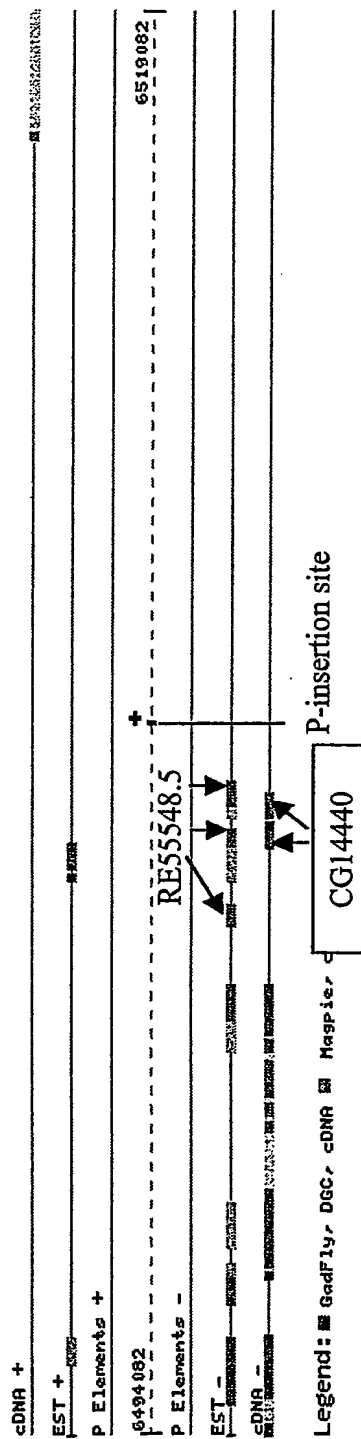


Figure 27. BLASTP results for CG14440 (GadFly Accession Number)**Homology to human protein NP_060000.1 (GenBank Accession Number)**

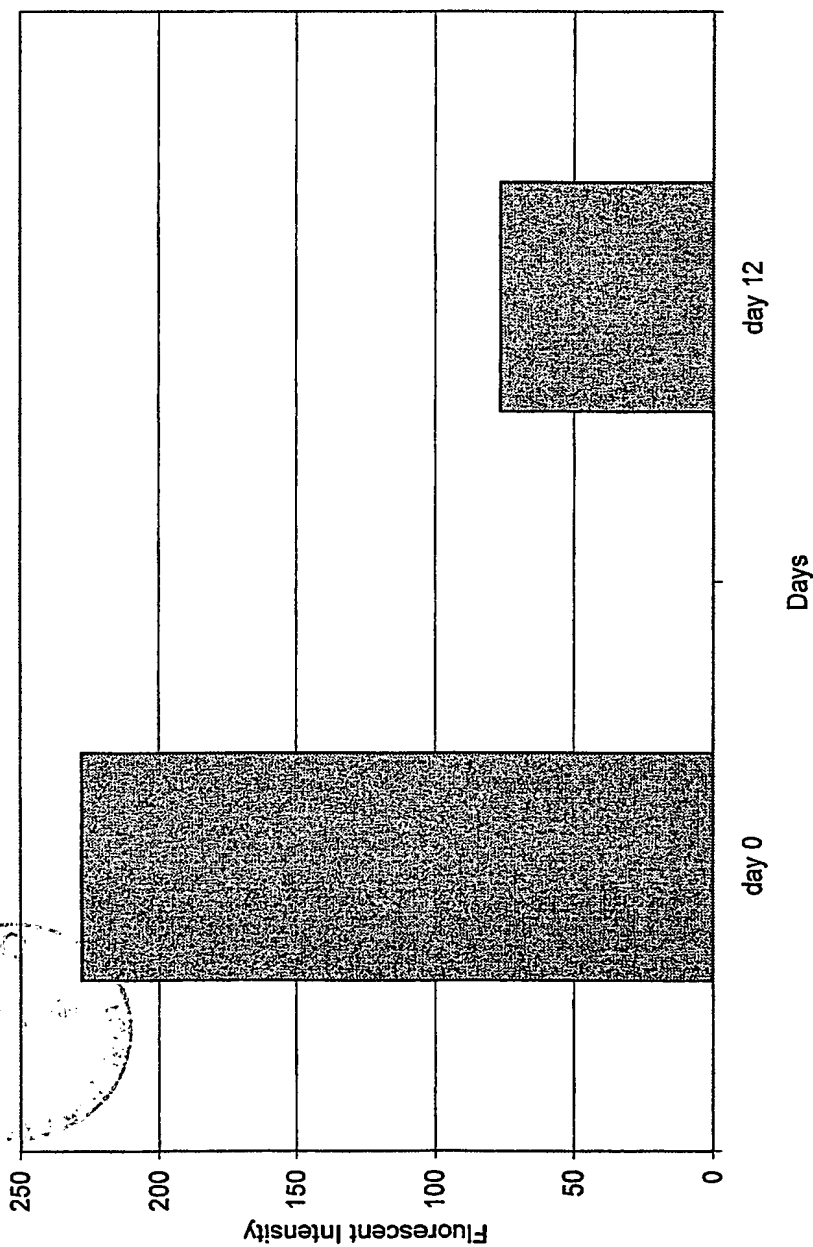
ref|NP_060000.1| (NM_017530) hypothetical protein LOC55565 [Homo sapiens]
Length = 370

Score = 77.4 bits (189), Expect = 2e-13
Identities = 41/106 (38%), Positives = 62/106 (57%)

Query: 195 QGQSSRAQKAARRRSNESIEARERRLERNAARMRDKRASEAEYRVRLAKNAEANRVRR 254
+ Q+ +K A RR NE +E R +RLER + +R E+ E VR ++ EA R++R
Sbjct: 207 EAQTPSVRKWALRRQNEPLEVRLQRLERERTAKKSRRDNETPEEREVRRMRDREAKRLQR 266

Query: 255 QNETEVQRTLRLMKNAARQRLRRASETVEERKKRLAKAAERMRIAR 300
ET+ QR RL ++ RL+RA+ET E+R+ RL + E R+ R
Sbjct: 267 MQETDEQRARRLQRDREAMRLKRANETPEKRQARLIREREAKRLKR 312

Figure 28. Expression of the human CG14440 homolog in mammalian (human) tissue
Quantitative analysis of human hypothetical protein LOC55565 expression in human abdominal adipocyte cells during the differentiation from preadipocytes to mature adipocytes



**This Page is Inserted by IFW Indexing and Scanning
Operations and is not part of the Official Record**

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images include but are not limited to the items checked:

- ☐ BLACK BORDERS
- ☐ IMAGE CUT OFF AT TOP, BOTTOM OR SIDES
- ☒ FADED TEXT OR DRAWING
- ☐ BLURRED OR ILLEGIBLE TEXT OR DRAWING
- ☐ SKEWED/SLANTED IMAGES
- ☐ COLOR OR BLACK AND WHITE PHOTOGRAPHS
- ☐ GRAY SCALE DOCUMENTS
- ☒ LINES OR MARKS ON ORIGINAL DOCUMENT
- ☐ REFERENCE(S) OR EXHIBIT(S) SUBMITTED ARE POOR QUALITY
- ☐ OTHER: _____

IMAGES ARE BEST AVAILABLE COPY.

As rescanning these documents will not correct the image problems checked, please do not report these problems to the IFW Image Problem Mailbox.